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Rao, Manjunath N.

Sent:

Thursday, September 26, 2002 11:05 AM

To: Subject: STIC-Biotech/ChemLib Sequence search request for 09/870,113

From: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10C 01

Phone: 306-5681

Date: 9-20-02

Please search the following as soon as possible for application with serial number 09/870,113

SEQ ID NO:3, 5,7,9,11, against all commercial nucleic acid databases including issued patents database and pending application database and provide a print of all results.

If y u have any questions please call me at the above phone number.

Thanks

Edward Hart Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Manjunath N. Rao, Ph.D. Biotechnology Patent Examiner Art Unit 1652, Room 10A11 Crystal Mall 1, USPTO.

Searcher:
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TYPE OF SEARCH:
NA Sequences:
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VENDOR/COST (where applic.) STN:
DIALOG:
Questel/Orbit:
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Homo sapi

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DVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRWQMYNSPYHRVTDCVRAVWQN
BAGAGAPYRSYTTQLTMNYPPGAIHPWYTEFLQEHFNPORRYNPSSHYLSGACAGAVAA
AATPELDVCKTLLMYPOSSLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIT
QIPSTAIAWSVYEFFKYLITKRQEEWRAGK
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                                                                                      ....c=":similar to mitochondrial RNA splicing protein 3/4;
alternatively spliced"
/ccdon_start=1
Li,F., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R. Larsson,C. and Suomalainen,A. Direct Submission

Submitted (08-DEC-2000) Human Molecular Genetics, National Public Health Institute, Mennerhelmintie 166, Helsinki 00300, Finland Location/Qualifiers
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Homo sapiens (human)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
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Larsson C., Suomalainen A.;
"Characterization of a novel human putative mitochondrial transporter
homologous to the yeast mitochondrial RNA splicing proteins 3 and 4";
FEBS Lett. 494:79-84(2001).
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/function="putative mitochondrial solute carrier"
/protein_id="CAC27996.1"
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LTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLL
NTOESLALNSHITGHTTGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYE
FFRYLITRROEEMRAGK H
FRYLITRROEEMRAGK H
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Life, Nikali, K, Gregan, J., Leibiger, I., Leibiger, B., Schweyen, R.,
Larsson, C. and Suomalainen, A.
Direct Submission
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1 i.j.F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R., Larsson,C. and Suomalainen,A.

Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing PERS Lett. 494 (1-2), 79-84 (2001)
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Euteleostomi;

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AL353719 123160 bp DNA linear PRI 25-SEP-2001
Human DNA sequence from clone RP11-85A1 on chromosome 10, complete
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 123160)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           aacaggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagac 473
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Lal,P., Yang,J., Yue,H., Hillman,J.L., Tang,Y.T., Bandman,O., Burford,N., Baughn,M.R., Azimzai,Y., Lu,D.A., Au-Young,J. and Patterson,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CGGGGGCCCGCCGCGCGGGGAGCCCGGGCCTGCAGGCCCCCGGTACGACAAGATCCGGA
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Pred. No. 1.3e-63;
                                                                                                                                                                  Human transport proteins
Patent: WO 0078953-A 76 28-DEC-2000;
Incyte Genomics, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                             267
                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
176 c 351 g 267
                                                                                                                                                                                                nomics, Inc. (US)
Location/Qualifiers
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               GI:12406365
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98.7%;
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                                                                                                                                                                                                                                                          /product="mitochondrial RNA splicing protein 3/4"
/function="putative mitochondrial solute carrier"
/protein_id="CAC27997.1"
/translation="MNPAEVVKQRWQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQL
TMNVPROAIHFMTYERLQBHFNPORRYNPSSHVLSGACAGAAAATTPLDVCKTLNT
QESLALNSHITGHITGMASAFRTVYQVGGVTAXFRGVQARVIYQIPSTAIAWSVYEFFR
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Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
                                                       Larsson C., Suomalainen A.;
Larsson C., Suomalainen A.;
"Characterization of a novel human putative mitochondrial transporter
homologous to the yeast mitochondrial RNA splicing proteins 3 and 4";
FEBS Lett. 494:79-84(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                             89.4%; Score 520.4; DB 17; 99.8%; Pred. No. 3.4e-74; ive 0; Mismatches 1;
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Sequence 76 from Patent WO0078953.
                                                                                                                                                                                                                /organism="Homo sapiens'
                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                    Location/Qualifiers
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/gene="HMRS3/4"
                                                                                                                                                                                                                                                                                                                                                       YLITKRQEEWRAGK"
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Matches 521; Conservative
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AC096351 221062 bp DNA linear HTG 20-DEC-2001 Rattus norvegicus chromosome Rfl clone CH230-24M6, WORKING DRAFT SEQUENCE, 33 unordered pieces.
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Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
Kalsam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pott, D.,
Lamson, G., Dramanac, R., Crkenjakov, R., Drmanac, S., Dickson, M.,
Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B.
Patent: WO 0102568-A 1912 11-3AN-2001;
CHIRON CORPORATION (US): HYSEQ; INC. (US)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
     91777 CCGGACTACGAGGCGCTGCCGGCTGGAGCCACTGTCACCACGCACATGGTGGCAGGCGCC 91718
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 1.6e-34;
                                                                                                                                                                                                                                       DNA
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100.0%; Pred. No. 1...
... 0; Mismatches
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                                                                                                                                                                                                                                             Sequence 1912 from Patent WO0102568.
AX071440
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/db_xref="taxon:9606"
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104 c 120
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Rattus norvegicus
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             Submitted (25-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Caudmitted (25-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk

On Sep 26, 2001 this sequence version replaced gi:14280413.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSENCY; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP that the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr10
RP11-85A1 is from the library RPCI-11.1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: PBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMPORTANT: This sequence is not the entire insert of clone RPI1-85A1 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RPI1-85A1 is at 1 in this sequence. The true left end of clone RPI1-85F11 is at 123601 in this sequence. The true right end of clone RPI1-129512 is at 51589 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91957 ATGGAGTTGGAGGGCGGGGTGCTGGCGGTGTGGCGGGGGGGCCCGGCGCGCGCGCGGGGGCCCGGG 91898
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Pred. No. 8.4e-38;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11.1"
complement(7066. .7118)
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Matches 291; Conservative
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/organism="Rattus norvegicus"
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RATURE S. B. TO 221062).

RATURE S. WARRY, D.W. Addama, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albbrooks, S. L., Amaretunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Blmage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burkett, C., Burrell, K.L., Byran, N.D., Buck, J., Burkett, C., Burrell, K.L., Byran, N.D., Burkett, C., Burrell, K.L., Byran, N.D., Burkett, C., Burrell, K.L., Byran, N.D., Durker, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Choedhry, I. Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Denn, A.L., Ding, Y., Durbin, K.J., Barnhart, C., Edgar, D., Ereber, H., Denn, A.L., Durp, M. H., Douthwaite, K.J., Draper, H., Denn, A.L., Durg, Y., Durbin, K.J., Earnhart, C., Edgar, D., Ereber, H., Denn, A.L., Durg, M. Falls, T., Ferraguco, D., Flagg, N., Ford, J., Forster, P., Frantz, P., Cablis, A., Gao, J., Garcia, A., Garner, T., Forster, P., Frantz, P., Cablis, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Goro, C., Harris, C., Harris, C., Harris, C., Harris, R., Harris, C., Harris, R., Harris, M., Hally, S., Hume, J., Jackson, E., Martindae, A., Martinez, E., Maresey, E., Mawhiney, E., Michell, N., Levis, R., Martinez, E., Massey, E., Mawhiney, E., Michell, T., Mohabat, K., Martinez, E., Wassey, E., Mawhiney, E., Michell, T., Mohabat, R., Mayen, N., Nuyyen, N., Nuyyen
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NOTE: This is a "working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (bases 1 to 221062)

Worley, K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Dec 20, 2001 this sequence version replaced gi:15627972.
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Consensus quality: 205303 bases at least Q30
Consensus quality: 209366 bases at least Q20
Consensus quality: 209866; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 3.9x in Q20 bases; sum-of-contigs estimation
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------ Summary Statistics
Assembly program: Phrap; version 0.990329First call to
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Center code: BCM
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. contig of 32851 bp in length contig of 16033 bp in length gap of unknown length contig of 14731 bp in length contig of 14731 bp in length contig of 12090 bp in length gap of unknown length contig of 12090 bp in length contig of 12736 bp in length contig of 12736 bp in length gap of unknown length gap of unknown length contig of 11011 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 6947 bp in length gap of unknown length gap of unknown length contig of 6947 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 7436 bp in length gap of unknown length bp in length bp in length bp in length bp in length in length bp in length length length ength length ength Length length Length length ength length ength ength length ength length ength. length ength contig of 2082 b gap of unknown l contig of 1385 b gap of unknown l unknown of 5575 7348 2358 9 219886: contig of 1428 77 219986: gap of unknown 7 221062: contig of 1076 Location/Qualifiers 6654 4950 unknown unknown unknown of 4785 4082 unknown 3702 3838 2179 2042 unknown 1569 unknown unknown contig of 1289 gap of unknown unknown unknown unknown unknown unknown unknown contig gap of gap of contig contig gap of contig gap of gap of contig contig gap of gap of contig gap of 49084: 88841: 88941: 08945 216969: 63815: 63915: 76005: 64028: 208845: 11802 44676 58878 29811

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Radio Margny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrach, Alsbrach, Alsbrach, Amargutunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binnage, R., Blankenburg, K., Bonnin, D., Bouck, J., Bouck, J., Blandae, K., Blankenburg, K., Bonnin, D., Bouck, J., Burch, P., Burkett, C., Burrell, K.L., Byrda, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrda, N.P., Carron, T.R., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., Davin, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgardo, O., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Eoster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garzer, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Hale, S., Hamilton, K. Harris, K., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratkovic, J., Lu, X., Lucier, R., Lucier, R., Lun, M., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Lucier, R., Lun, R., Martinez, E., Massey, E., Martinez, C., Matchen, N., Morse, M., Marse, M., Morse, M., Morse, M., Marse, M
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Rattus norvegicus chromosome Rfl clone CH230-24M6, WORKING DRAFT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72925 CGGAGCCCCGGGGAGTCGGCGGTGCTGGACGGGTGCTGCAGCGGGGCGTGGCCCGGGGG 72984
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                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                           3487 others
                                                                                                                                                                                                                                                                                                                 25; Indels
                                                                                                                                                                                                                                             Score 251; DB 2;
Pred. No. 1.9e-31;
0; Mismatches 25;
                                                                    /clone="CH230-24M6"
50577 c 49732 g 58877 t
/db_xref="taxon:10116"
/chromosome="Rf1"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                         43.1%;
ilarity 91.4%;
Conservative
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Rattus norvegicus
                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                             Query Match
Best Local s
                                                                                                    BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is
Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, T., Rolfe, M., Suison, I., Soherer, S., Scott, G., Shen, H., Shoshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tansey, J., Taylor, C., Taylor, P., Yalladon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wall, R., Mulliams, G., Williamson, A., Wleczyk, R., Wooden, S., Weinstock, G. and Gibbs, R., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There is a second of the secon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 200164 bases at least Q40
Consensus quality: 203303 bases at least Q30
Consensus quality: 209366 bases at least Q30
Estimated insert size: 209880; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 3.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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of 10862 bp in length
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Center project name: GEZD
Center clone name: CH230-24M6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
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ROD 27-0CT-2001

SW

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/translation="MELRRGGVGNQAAGRRMDCDCRDGGCGSKDAGSEDYENLPTSAS
VSTHMTAGAMAGILEHSIMYPVDSVKTRMQSLNPDPKARYTSIYGALKRIMHTEGFWR
PLRGLNVMMMGAGPAHAMYFACYENMKRTLNDVFSHQGNSHLANGVAGSMATLLHDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNPAEVVKORLOMY NSQHQSAFSCIRTVWRTEGLGAFYRSYTTOLTMNIPFOSIHFIT
YEFLOBQVNPRRDY NPQSHIISGGLAGALAAAATTPLDVCKTLLNTOENMALSLANVS
GRLSGMANAFRTVYOLNGLAGYFKGIQARVIYOMPSTAISWSVYEFFKYILTKROLEN
                                                                                                                                                            Li,Q.-z., Ruan,Q.-G., Eckenrode,S., Shi,J.-D., Cruz,P., Wang,C.-Y. and She,J.-X.
                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                     Submitted (20-JUL-2000) Pathology, University of Florida, 1600 Archer Road, Rm. D6-15, Gainesville, FL 32610, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 gaggecegggectgeaggeceeeggtacgacaagateeggaeteeggeee---ggaetae 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 GCGGGCCGCGGGATGGAGCTCCGCCGTGGCGCGTGGGGAACCAGGCTGCGGGCCGGAGG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 ATGGATGGGGACTGCCGCGATGGCGGCTGCGGCAGCAGGACGCCGGGTCGGAGGACTAC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 atcctggagcactgcgtgatgtaccccatcgactgcgtcaagacccggatgcagagtcta 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 AATCCAGATCCCAAAGCCCGGTATACAAGCATCTATGGCGCCCTCAAGAGGATCATGCAC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 acggagggcctatggaggcccatgagggggctgaacgtcacagcaacaggcgcagggcct 429
                                                                                                                                                                                                                                                                                                                                                                                      /product="mitochondrial solute carrier-like protein"
/protein_id="AAL23859.1"
/db_xref="G1:16506178"
Muswills mitochondrial solute carrier-like protein mRNA, AF288621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 207.2; DB 10; Length 4112; Pred. No. 3.7e-24; 0; Mismatches 178; Indels 3;
                                                                                                                                                                         A new gene which is highly expressed in NOD mice spleen Unpublished
                                                                                                                                                                                                        2 (bases 1 to 4112)
Li,O.-Z., Shi,J.-D., Cruz,P., Echenrode,S., Ruan,Q.-G.
Wang,C.-Y.
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                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
116. :1132
                                                                                                           Mus musculus
Bukaryota; Metazoa; Chordata;
Bummalia; Butheria; Rodentia;
1 (bases 1 to 4112)
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/note="50E12"
/codon_start=1
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ilarity 64.4%;
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/db_xref="taxon:10116"
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Best Local Similarity 94.0
Matches 219; Conservative
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/translation="MELRRGGVGNQAAGRRMDGDCRDGGCGSKDAGSEDYENLPTSAS VSTHMTAGAMAGILEHSIMYPVDSVKTRMQSLNPDPKARYTSIYGALKRIMHTBGFWRPLKGLNVMMAGAGPAHAMYFACYENWKRTLNDVFSHQGNSHLANGILKAFVWSWEALL
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SW Archer Road,
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Li,Q., Eckenrode,S., Wang,C., Ruan,Q., Shi,J., McIndoe,R.A.
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/evidence=not_experimental
/product="mitochondrial carrier-like protein"
/db_xref="G1:1675528"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-MAR-2001) Department of Pathology, Laboratory Sciences, University of Florida, 1600 Room D6-15, Gainesville, FL 32610, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="between D14Mit124 and D14Mit236"
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Pred. No. 1.7e-19;
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/strain="C57BL/6J"
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1 (bases 1 to 5869)
Li,Q., Eckenrode,S., Wang,C.,
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/note="MCLP"
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/product="H015 protein"
/protein_id="AAF6411.1"
/protein_id="AAF6411.1"
/protein_id="C1:7578783"
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A novel gene expressed in human hypothalamus
Unpublished
2 (bases 1 to 1429)
Song, H., Gao, G., Peng, Y., Ren, S., Chen, Z. and Han, Z.
Direct Submission
Submitted (12-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1429)
  GCGCACGCCATGTATTTTGCCTGCTATGAAAACATGAAAAGGACTTTAAATGACGTTTTC 523
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Homo sapiens HT015 protein (HT015) mRNA, complete cds.
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llarity 62.7%; Pred. No. 9.6e-23;
Conservative 0; Mismatches 192;
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/db_xref="taxon:9606"
/tissue_type="hypothalamus"
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Li,O.-Z., Eckenrode,S., Ruan,Q.-G., Wang,C.-Y., Shi,J.-D., McIndoe,R.A. and She,J.-X.
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SW Archer Road,
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                          gagteggegetgetggaegggtggetgeagegggggegtgggeeggggggeeggeggeggg 132
                                                                            gaggeceggggectgeaggececeggtaegaeaagateeggaeteeggeee---ggaetae 189
                                                                                                                                                    404 ACTGAAGGCTTCTGGAGGCCCCTGCGGGCCTGAACGTGATGATGGGTGCAGGGCCC 463
                                                 GCGGGGCCGCGGATGGAGCTCCGCCGTGGCGCGTGGGGAACCAGGCTGCGGGCCGGAGG 163
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Laboratory Sciences, University of Florida, 1600
Room D6-15, Gainesville, Florida 32610, USA
Location/Qualifiers
Mismatches 162;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
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Li,Q.-Z., Eckenrode,S., Ruz
McIndoe,R.A. and She,J.-X.
Direct Submission
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/gene="MSCP"
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/product="mitochondria solute carrier protein"
/protein_id="AAX18154_1"
/brotein_id="1377418154_1"
/d_xref="dI:137741819"
/translation="MERESGSWGSQAVARRMDGDSRDGGGGKDATGSEDYENLPTSAS VSTHWTAGAMAGILEHSVWYPVDSVKTRWQSLSPDPKAQYTSIYGALKKIMRTEGFWRPLRGYVWMMGAGPAHAMYFACYENWKRTLNDVFHHQGNSHLANGILKAFVWS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3415;
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IMAGE:3910567, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 174.2; DB 9;
Pred. No. 7.1e-19;
; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
1 (bases 1 to 858)
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BC015013
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                                                                                                                                                                                                                                                                                                                       851 c
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Direct Submission
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* NOTE: Estimated insert size may differ from sequence length
                         Rattus norvegicus
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                                                                                           Rattus.
                       ORGANISM
                                                                                                                REFERENCE
                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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SOURCE
                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 15 Row: h Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7706149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MELRSGSVGSQAVARRMDGDSRDGGGGKDATGSEDYENLPTSAS
YSTHWTAGAMAGILEHSVMYPVDSVRRRMQSLSPDPRAQYTSIYGALKKIMRTEGFWR
PLRCVNVMIMGAGPAHAMYRACYENMKRTLNDVFHHQGNSHLANGILKAFVWS"
220 c 231 g 192 t
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                  Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chia, Readman Chia, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Sess, Pawarn Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus clone CH230-84G11, *** SEQUENCING IN PROGRESS AC099368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgccgt 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 GGCCGGGATCCTGGACCACTGGTCATGTACCCGGTGGACTCGGTGAAGACACGAATGCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tataagaacggaaggcctatggaaggcccatgaagggggctgaacgtcacagcaacaggcgc 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 agggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattgagtga 482
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ive 0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Unknown (protein for MGC:8764)"
/protein_id="AAH15013.1"
/db_xref="GI:15929110"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71"
/lab_host="DH108"
                                                                                                                                                                            George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 tgtaatccaccctgggggcaatagccatattgccaatggt 522
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                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="MGC:8764 IMAGE:3910567"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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HTG; HTGS_PHASE1.
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  info@bcgsc.bc.ca
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Best Local Similarity
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ORIGIN
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RS Muzny, D. M., Adams, C., Adio-Oducla, B., Ali-osman, F. R., Allan, C., Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Banks, T., Barbaria, J., Babrooks, S. L., Amaratunge, H. C., Are, J. R., Banks, T., Barbaria, J., Burdon, O., Blimage, K., Blankenburg, K., Bondin, D., Bouck, J., Burda, M., Bryant, N. P., Buhay, C., Burch, P. Buhay, C., Burch, P., Burda, M. C., Carron, T. F., Carter, M. Carter, Dedovo, J., Carter, Davis, C., Davy, Carroll, L. Dedovo, J., Carter, C. Edgar, D. Edwards, C. Coyle, M. J. Delaney, K. R., Delaney, K. R., Delaney, K. R., Delaney, K. R., Dugan-Rocha, S., Durbin, K. J., Earnhart, C., Edgar, D., Edwards, C. Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Forster, P., Frantz, P., Gablis, A., Gao, J., Gartca, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hacks, J., Harnandez, J., Hernandez, J., Hulber, J., Hulyk, S., Hume, J., Joudah, S., Karlsson, E., Jacobson, B., Jar, Y., Johnson, R., Jollow, M., Li, Z., Lidhtage, O., Lieu, C., Liu, J., Li, Z., Lidhtage, O., Lieu, C., Liu, J., Li, Z., Lidhtage, C., Liu, K., Liu, R., Howsen, M., Marlis, S., Moser, M., Marlia, B., Martine, E., Maccholl, J. Martin, M. Marlis, S., Moser, M., Morgan, M., Rajue, M., Stanley, H., Sutcon, B., Stone, H., Sutcon, A., Sateke, M., Tabor, P., Tamerisa, A., Stanley, M., Tangyen, C., Taylor, C., Tang, M., Morley, K., Wu, Y., Wu, Ten, M., Walliams, G., Waller, C.
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Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Phrap; version 0.990329First call to
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Web site: http://www.hgsc.bcm.tmc.edu/
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------ Project Information
Center project name: GHIJ
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Direct Submission
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
             NOTE: This is a "working diraft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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(HUMA-) HUMAN GENOME SCI INC.

Human polynucleoti	Human mitochondria	Human bone marrow	Human immune/haema	Human full-length	Human cDNA 5'-end	Human cDNA clone r	Human full-length	Human ORFX ORF2730		Human cDNA 5'-end	Human cDNA clone r	Human bone marrow	Human secreted pro	Human secreted pro	Human ORFX ORF2744	Human gene express	Human gene express	Human immune/haema	Mouse ischaemic co	Aspergillus oryzae	Drosophila melanog	Human immune/haema	Human ORFX ORF2729	Human colon cancer	Human polynucleoti	nsed in	Primer used in the	2	Human IL-1ra BAC c	cDNA sequence #574	Primer used in the	DNA encoding novel	DNA encoding novel	Primer used in the	Mouse ischaemic co
AAK52172	AAF59920	AAH90057	AAK58672	AAK94897	AAK92357	AAK93895	AAK94871	AAC77175	AAC91320	AAK91764	AAK93200	AAH89944	AAV84573	ABA83356	AAC77189	AAZ13026	AAZ15876	AAK80493	AB199871	AAF12614	ABL08627	AAK83876	AAC77174	AAA02484	AAI84504	AAA38184	AAA38186	AAZ77506	AAX02974	AAS62787	AAA38185	AAS84408	Ч	긆	ABI99656
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ALIGNMENTS

uncoupling protein; immunosuppressive; antiarthritic; leumatic; antiproliferative; cardiant; vasotropic; proprotective; neuroprotective, antibacterial; opthalmological; protestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; herapy; cancer; wound; infectious disease; thrombosis; arthritis; illty; ss. uncoupling protein cDNA #6. 99US-0128701. 99US-0142821. 99US-0149448. 99US-0164751. 06-APR-2000; 2000WO-US09534. -2001 (first entry) WO200061614-A2. 09-APR-1999; 08-JUL-1999; 18-AUG-1999; 12-NOV-1999; Homo sapiens. 19-OCT-2000. ~

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Local
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                                                                                                                    The present sequence is one of eighteen isolated nucleotide sequences encoding uncoupling proteins. The nucleotide sequences may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
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                                                                                                                                                                                                                                                                                     Gaps
                                                      Uncoupling proteins and nucleic acid sequences encoding them, useful
                                                               for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders
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 Rosen CA, Soppet DR;
                                                                                                                                                                                                                               Sequence 1336 BP; 333 A; 377 C; 358 G; 268 T; 0 other;
                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                             Score 469.4; DB
Pred. No. 2e-85;
0; Mismatches
                                                                                               Claim 1; Page 306-307; 343pp; English.
Ni J, Komatsoulis G,
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99.8%;
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Matches 470; Conservative
                    2000-656322/63.
                              P-PSDB; AAB50383
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immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiniflammatory; antiviral; antibacterial; antimitumatory; antiviral; antibacterial; antifungal; antithyroid; antiantanemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antithflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy
anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vectors. The proteins and nucleic acids may be used to treat cancers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences for 43 novel human transport proteins (designated TPPTs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative
                                                                                                                                                                                                                                                                                                          Human; transport protein; TPPT; transport disorder; metabolic disorder;
neurological disorder; cardiovascular disorder; reproductive disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide with a human transport protein sequence is use; for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular systems
                                                                                     cagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctggagg
                                                              giggeagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaagacccggatg
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Patterson
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Lu DAM, Au-Young J,
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                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                            standard; cDNA; 1322
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99US-0148177.
99US-0149357.
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1mmune disorder; cancer; ss.
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                                                                                                                                                                                                                                                                           (first entry)
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Azimzai Y,
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P-PSDB; AAB60113.
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18-AUG-1999;
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Baughn MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; curspathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                   2 cggggggccggcgcgggggaggccggggcctgcaggcccccggtacgacaagatccgga 61
                                                                                                                                                                                                                                                                                                                            ccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccct
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0
                                                                            22; Length 1322;
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                              T; 0 other;
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9
                                                                        Score 454.4; DB Pred. No. 2e-82; 0; Mismatches
                              267
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G
                              C; 351
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                              BP; 328 A; 376
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0652450.
2000US-0662191.
                                                                        78.1%;
Similarity 98.7%;
58; Conservative
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disorders such as cancer
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                              Sequence 1322
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
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Matches 458;
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                                                                                                                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                              system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotectic/chemokinetic activity, heamotectic/chemokinetic activity, heamotectic/chemokinetic activity, heamost and thrombolytic activity, cancer diagnosis and therapy, duug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                               C.N.§ disorders. Note: The sequence data for this patent did not form part of the printed
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                                                           Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 gcactgcgtgatgtaccccatcgactgcgtcaagacccggatgcagagtctacagcctga
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Zhang J;
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                                                          Qian XB,
Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.6%; Score 440; DB 22;
100.0%; Pred. No. 1.5e-79;
ive 0; Mismatches 0;
                                                          Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                               Claim 1; SEQ ID NO 4650; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agccatgaaccctgcggaag 577
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
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                                                                                                          WPI; 2001-442253/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 440; Conserv
                                   (HYSE-) HYSEQ INC
                                                                                                                     P-PSDB; AAM41505
                                                          Tang YT,
Wang J, W
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
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Sequences AASO3873-AASO3922 represent isolated nucleic acid molecules and PCR primers of the invention. acid of the invention. Secreted proteins and their related nucleic acids can be used in the diagnosis of or susceptibility to a pathological condition by determining the presence or absence of a mutation in a nucleic acid or the presence or amount of a secreted protein. The sequences are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The antibodies to the polypeptides can also be used in alleviating symptoms associated with disorders and in diagnostic immunoassays or enzyme linked immunosorbent assays (ELISA). The disorders include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. choplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The peptides can also be used to aid wound healing and epithelial cell proliferation, to help prevent skin ageing due to sunburn, to maintain organs before transplantation, to regenerate tissues, in chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein; autoimmune disorder; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forty one nucleic acid molecules encoding human secreted proteins, useful the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; bacterial infection; viral infection; ss; fungal infection; coular disorder; wound healing; tissue regeneration; epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
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                                                                                                                                                                                                                                                                                                    Human secreted protein gene #25.
                                   AAS03906 standard; cDNA; 2502
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Matches 412; Conserv
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AGCCATGAACCCTGCGGAAG 855

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humenostatic; amyotrophic lateral scleroals; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Ren F,
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Yang Y,
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Xu C, Xue AJ,
t, Drmanac RT;
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Wehrman T, Xu
Goodrich R,
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19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
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2000US-0552317.
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Wang Z, W
Zhou P,
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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Hutington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, chemoteactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                    the sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                           cggggcctgcaggcccccggtacgacaagatccggactccggcccggactacgaggcgct 197
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Pred. No. 3.1e-71;
0; Mismatches 19; Indels 1;
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grancer; cancer detection; s
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Best Local Similarity 95.5%;
Matches 421; Conservative
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cancer; lung
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Note: The sequenc
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24591.
                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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2000US-0224518.
2000US-022519.
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2000US-025214.
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2000US-0198123.
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2000US-0215135.
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2000US-0227009.
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2000US-0226279
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16-MAR-2000;
17-MAR-2000;
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14-AUG-2000;
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22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2000;
22-AUG-2000;
06-NOV-2001
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30-AUG-2000;
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    \texttt{C} \times 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonaleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                          Garcia PD, Klinger J, Kassam A;
Pot D, Lamson G, Drmanac R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 ggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattgagtgatg 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                               Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmana
Crkenjakov R, Drmanac S, Dickson M, Labat I, Leshkowitiz D;
Kita D, Garcia V, Jones LW, Strache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tacttcatgatgcagccatgaaccctgcggaag 577
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                                                                                                                                                                                                                                                                                                                                                                                                          Escobedo J, Innis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 818; 1046pp; English.
                                                                                                                                                         99US-0142310.
99US-0142311.
                                                                              30-JUN-2000; 2000WO-US18374
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Reinhard C,
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02-JUL-1999;
11-JAN-2001
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Query Match Best Local S

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2000US-0233063

14-SEP-2000; 14-SEP-2000;

AAK69779 standard; DNA; 27960 BP

AAK69779

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2000US-0237037.
2000US-0237038.
2000US-0237039.
2000US-0237040.
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2000US-0241826.
2000US-0244617.
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2000US-0251868
                  21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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20-OCT-2000;
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01-NOV-2000;
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17-NOV-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
corrections and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
correction of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
collynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
polynucleotides and polynucleotides may be used to prevent,
clagnose and treat immune/haematopoietic-derived cells. AAK64703
concers and cancer metastases of haematopoietic-derived cells. AAK64703
concers and cancer immune/haematopoietic antigen genomic
sequences from the present invention. AAK64942 to AAK64960 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18383 ggcccatgagggggctgaacgtcacagcaacaggcgcagggcctgcccacgccctttatt 18442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggcccatgaggggctgaacgtcacagcaacaggcgcagggcctgcccacgccctttatt 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28132.
                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 24591; 3071pp + Sequence Listing; English.
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                                                                                                                                                   Ruben SM;
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                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                 08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
 2000US-0251869
                                                                        05-JAN-2001; 2001US-0259678
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Matches 242; Conservative
                                                                                                                                                   Barash SC,
                                                                                                                                                                                     WPI; 2001-483426/52
                                                                                                                                                   Rosen CA,
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                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0180628.
2000US-018664.
2000US-0189874.
2000US-0199123.
2000US-020515.
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2000US-0215135.
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23-AGG-2000;

23-AGG-2000;

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14-SEP-2000;
21-SEP-2000;
                                                                            Homo sapiens.
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20000S-0249245. 20000S-0249245. 20000S-0249295. 20000S-0249299. 20000S-02599. 20000S-0250160. 20000S-02501988. 20000S-0251988. 20000S-0251868. 20000S-0251868. 20000S-0251869. 20000S-0251869.

20000S-0234998 20000S-0235848 20000S-0235834 20000S-0235836 20000S-0235836 20000S-0235836 20000S-02353630 20000S-02353630 20000S-02353630 20000S-0237033 20000S-0237033 20000S-0237039 20000S-0237039 20000S-0237039 20000S-0241221 20000S-0241809 20000S-0241809 20000S-0241809 20000S-0241809 20000S-0241809 20000S-0241809 20000S-0241809 20000S-0241809 20000S-0241809 20000S-024617 20000S-024617 20000S-024652 20000S-024652

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tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                       WO200157190-A2
                                                                                                 09-AUG-2001
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                                                                                                                                                                                                        AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
concers and cancer metastases of haematopoietic antigen genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention
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                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18323 cccgctatcgcaatgtgttggaggccctctggaggattataagaacggagggcctatgga 18382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18383 ggcccatgaggggggtgaacgtcacagcaacaggggcgcagggcctgcccacgccctttatt 18442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18443 ttgcctgctacgaaaagttaaaaaagacattgagtgatgtaatccaccctgggggcaata 18502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgatgtaccccatcgactgcgtcaagacccggatgcagagtctacagcctgacccagctg 325
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                                                                                                                                                                                 Disclosure; SEQ ID NO 28132; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
40.0%; Score 233; DB 22; Length 27960;
Best Local Similarity 94.2%; Pred. No. 5.6e-38;
Matches 242; Conservative 0; Mismatches 15; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27960 BP; 7998 A; 5835 C; 6583 G; 7544 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 717.
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                                         (HUMA-) HUMAN GENOME SCI INC.
11-DEC-2000; 2000US-0254097. 05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 gccatattgccaatggt 522
                                                                     Barash SC,
                                                                                                WPI; 2001-483426/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                          metastasis
                                                                     Rosen CA,
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1040 ctgcgccccgccgagctggcggatggagctgcgcagcgggagcgtgggcagccaggcggt 1099
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ang J, Ren F, Chen R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Length 1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 200.4; DB 2 Pred. No. 1.7e-31;
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Wejhrman T, Goodrich R;
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                                                            03-FEB-2000, 2000US-0496914.
27-APR-2000; 2000US-0566B75.
20-JUN-2000; 2000US-058075.
19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-064936.
15-SEP-2000; 2000US-064936.
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62.9%;
05-FEB-2001; 2001WO-US04098
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                             30-NOV-2000;
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cgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattgag gattataagaacggaggcctatggaggcccatgagggggttgaacgtcacagcaacagg ondrial solute carrier protein; hMSC-o; hypothalamus; detection; ss. Human mitochondrial solute carrier protein hMSC-o cDNA HUMAN GENE GROUP. BP. AAF59920 standard; cDNA; 1305 (SREN-) SOUTHERN RES CENT NAT 17-MAR-2000; 2000CN-0114958 17-MAR-2000; 2000CN-0114958 (first entry) Gao X, Xiao WPI; 2001-050544/07. mitochondrial P-PSDB; AAB60658 preparation; Homo sapiens 04-MAY-2001 CN1269409-A. 11-OCT-2000 Zhang X, AAF59920; Human 1280 420 480 360 q 8 ŏ ð ò

The invention relates to a novel human mitochondrial solute carrier protein, hMSC-o (AAB60658), and cDNA encoding it (AAF59920). hMSC-o is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-o proteins and nucleic acids, and the detection of hMSC-o proteins and nucleic acids, in a sample. The present sequence represents cDNA encoding hMSC-o. New human mitochondrion solute carrier protein and its nucleic acid Claim 1; Page 19-20; 21pp; Chinese.

Sequence 1305 BP; 292 A; 388 C; 363 G; 262 T; 0 other;

Length 1305;

DB 22;

Query Match

ó ggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgccgt 242 ggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaagacccggatgca 302 33.8%; Score 196.6; DB 2; 68.6%; Pred. No. 9.5e-31; iive 0; Mismatches 124; Conservative Best Local Similarity Matches 271; Conserv 243 183 57 q ò ò

tgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtggcaac 542 357 cyttttccaccaaggaaacagccacctagccaacgggatagctgggagtatggccac 416 Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders gagtetacageetgaeeecagetgeeegetategeaatgtgttggaggeeetetggaggat gagtttgagtccagatcccaaagcccagtacacaagtatctacggagccctcaagaaaat tataagaacggaggcctatggaggcccatgaggggggctgaacgtcacagcaacaggcgc V, Chen R, Ma Yang Y, Zhang J; The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the Asundi V, 3J, Tang YT, Liu C, Asundi Werhman T, Xu C, Xue AJ, 543 attacttcatgatgcagccatgaaccctgcggaag 577 Human bone marrow cDNA, SEQ ID NO: 301. Claim 1; Page 412-413; 648pp; English. ВР Zhou P, Drmanac RT; AAH90057 standard; cDNA; 2562 2000US-05488725. 2000US-055317. 2000US-0598042. 2000US-0653150. 2000US-0653450. 2000US-0653450. 2000US-0653450. 2000US-0653450. 23-DEC-2000; 2000WO-US34960 (first entry) 2001-488707/53 Boyle BJ, (HYSE-) HYSEQ INC WPI; 2001-488707, P-PSDB; AAM00938 WO200153453-A2 03-AUG-2000; 14-SEP-2000; 30-NOV-2000; Homo sapiens 21-JAN-2000; 25-APR-2000; 09-JUL-2000; 19-JUL-2000; 19-OCT-2000; Wang 01-OCT-2001 26-JUL-2001 AAH90057; JĒ, Zhao QA, Ford 177 363 237 297 483 117 303 423 AAH90057 qq ŏ Q ò à q ŏ g ò g

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14-AUG-2000; 2000US-0225214.
14-AUG-2000; 2000US-0225266.
14-AUG-2000; 2000US-0225267.
14-AUG-2000; 2000US-0225267.
14-AUG-2000; 2000US-0225270.
14-AUG-2000; 2000US-0225447.
14-AUG-2000; 2000US-0225447.
14-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-0225759.
22-AUG-2000; 2000US-02257182.
23-AUG-2000; 2000US-02257182.
23-AUG-2000; 2000US-02257182.
23-AUG-2000; 2000US-02257182.
23-AUG-2000; 2000US-02257182.
23-AUG-2000; 2000US-02257182.
23-AUG-2000; 2000US-0229344.
01-SEP-2000; 2000US-0229345.
05-SEP-2000; 2000US-0229345.
06-SEP-2000; 2000US-0229314.
06-SEP-2000; 2000US-0229314.
06-SEP-2000; 2000US-0229314.
06-SEP-2000; 2000US-0231243.
06-SEP-2000; 2000US-02311414.
08-SEP-2000; 2000US-02311414.
08-SEP-2000; 2000US-02311414.
08-SEP-2000; 2000US-02311414.
08-SEP-2000; 2000US-02311414.
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2000US-0216647.
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2000US-0217487.
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2000us-0231968.
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2000US-0214886
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2000US-0218290
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2000US-0237039
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                                              2000US-0198123
                   16-MAR-2000; 2
17-MAR-2000; 2
19-MAY-2000; 2
19-MAY-2000; 2
07-JUN-2000; 2
30-JUN-2000; 2
07-JUL-2000; 2
11-JUL-2000; 2
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14-JUL-2000; 2
26-JUL-2000; 2
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14-AUG-2000; 2
14-AUG-2000; 2
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polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation. suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                     2160 ccatgtattttgcctgctatgaaaacatgaaaaggactttaaatgacgttttccaccacc 2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2220 aaggaaacagccacctagccaacgggatagctgggagtatggccaccctgctccacgatg 2279
                                                                                                                                                                                                                                                                                                                                                                                                317 acccagctgcccgctatcgcaatgtgttggaggccctctggaggattataagaacggagg 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3732
                                                                                                                                                                                                                              Query Match 32.2%; Scoré 187.4; DB 22; Length 2562; Best Local Similarity 68.2%; Pred. No. 6.9e-29; Matches 260; Conservative 0; Mismatches 121; Indels 0;
                                                                                                                                                                                        Sequence 2562 BP; 623 A; 660 C; 627 G; 652 T; 0 other;
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) are amino acid sequences given in AAW82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic companies from the present inwention. AAK64902 to AAK84950 and AAM82169 represent theman immune/haematopoietic antigen genomic sequences from the present invention. AAK64912 to AAK84950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cctctggagagtattataagaacggaggcctatggaggcccatgagggggctgaacgtcac 410
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                                                                                                                                                                                                                                                                                                                                                                                  31.1%; Score 181; DB 22; Length 339; 95.1%; Pred. No. 1.2e-27; Live 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                   Sequence 339 BP; 86 A; 84 C; 101 G; 64 T; 4 other;
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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Matches 195; Conservative
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2000US-0246527
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P-PSDB; AAM85891.
                              13-0CT-2000;
20-0CT-2000;
20-0C
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H; Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga Human; full length cDNA; cDNA synthesis; oligo-capping; ss. WPI; 2001-524255/58 us-09-870-113-3.rng

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-bads of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length were income.
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                                     and their
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specification, but was obtained in CD-ROM format directly from EPO
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                                                                                                                                                                                                                                                                                                                                                                                           Length 1890;
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                               830 Primers useful for synthesizing full length cDNA clones
                                                                                   Claim 8; SEQ ID NO 4109; 1380pp + sequence listing; English
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62.4%;
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                                                   in genetic manipulation
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Best Local Similarity 62.4
Matches 289; Conservative
 AAM93934
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been soluted and nucleotide sequences of 5'— and 3'—ends of the CDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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K, Kojima S, Otsuki T, Koga
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0; Mismatches 104; Indels
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2000JP-0118774.
2000JP-0183765.
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69.4%;
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Best Local Similarity 69.4
Matches 236; Conservative
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02-MAY-2000;
               EP1130094-A2
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Search completed: September 28, 2002, 08:05:43 Job time: 11538 sec

36, Appl 1, Appli 1, Appli 1, Appli 11, Appli 1, Appli

15, Appl 1, Appli 3, Appli 7, Appli

Sequence Seq

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gagccccgggggagtcggcgctgctggacgggtggctgcagcgggggcgtgggccgggggggc 122
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Pred. No. 8.5e-06;
O; Mismatches 56;
US-09-283-471A-39
US-08-658-136-2
US-08-4658-136-1
US-08-283-471A-36
PCT-US91-06532-1
US-08-118-06532-1
US-08-118-06532-1
US-08-458-745-1
US-09-458-568A-11
US-09-45-283-1
US-09-773-816-1
US-09-773-816-1
US-09-773-816-1
US-09-775-8918-24
US-09-236-097-7
US-09-236-097-7
US-08-658-8838-1
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US-08-658-8838-1
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CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 8
LENGTH: 319
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Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
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Sequence 8, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 63.2%;
Matches 96; Conservative
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   US-09-165-264-12
   TYPE: DNA
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Sequence 1,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 version 4.5
- 2000 Compugen Ltd
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US-09-165-264-11
US-08-403-11
US-08-510-646B-3
US-08-231-818-3
US-08-231-818-3
US-08-231-818-1
US-09-231-818-1
US-08-231-818-1
US-08-931-818-1
US-08-931-818-1
US-08-904-227C-1
US-08-904-23
US-08-690-473-1
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US-08-6843-659-1
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US-09-165-264-14
US-09-128-155-16
US-09-165-264-7
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US-09-103-840A-1
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US-08-903-800A-4
US-08-483-533-39
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Maximum Match 100%
Listing first 45 summaries
                                                                             nucleic search, using sw model
                                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                 GenCore
Copyright (c) 1993
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length: 2000000000
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Description of Artificial Sequence: Primer sequence US-09-165-264-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                         10.0%; Score 58.2; DB 4; Length 318; 61.6%; Pred. No. 7.4e-05; tive 0; Mismatches 58; Indels (
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Pred. No. 7.4e-05;
0; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OE INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 14
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 ggcagggatcctggagcactgcgtgatgtaccccatcga 281
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US-09-165-264-14
Sequence 14, Application US/09165264
Patent No. 6197510
                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 50.5%;
Matches 141; Conservative
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Best Local Similarity
Matches 93; Conserva
              LENGTH: 318
SEQ ID NO 12
                                                       FEATURE:
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GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION:
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT PILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER PLING DATE: 1998-07-02
EARLIER PLING DATE: 1998-07-02
EARLIER PILING DATE: 1998-07-03
SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15-03
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US-09-165-264-7
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Sequence No. 6197510

GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVERTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747

CURRENT APPLICATION NUMBER: US/09/165,264

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 7

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
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Pred. No. 0.0002;
0; Mismatches 93;
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Pred. No. 9.1e-05;
0; Mismatches 57;
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Sequence 16, Application US/09128155 Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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TYPE: DNA
ORGANISM: Artificial Sequence
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55.1%;
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Best Local Similarity 55.1<sup>s</sup>
Matches 114; Conservative
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Best Local Similarity 61.7
Matches 92; Conservative
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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US-09-165-264-7
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Sun Sep 29 09:07:54 2002

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ORGANISM: S.pristinaespiralis

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APPLICANT: Thibaut, news.
APPLICANT: Zagorec, Monique
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: Debussche, Laurent
APPLICANT: De Creoy-Lagard, Valerie
APPLICANT: Aguences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
                                                                                                                                                    63 gagccccgggggagtcggcgctgctggacgggtggctgcagcgggggcgtgggccggggggc 122
                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
  Pred. No. 0.00011;
0; Mismatches 56;
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REGISTRATION NUMBER: 25,146
REFERENCE/POCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/403,852D FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
                                                                                                                                                                                                                                       123 cggcggcgggaggccggggcctgcag 149
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; Patent No. 5891695
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Lacroix, Patricia
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Crouzet, Joel
  61.98;
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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LENGTH: 833 base pairs
  Best Local Similarity 61.9
Matches 91; Conservative
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ZIP: 20005-3315
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                   US-08-403-852D-3/c
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                                      Gaps
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-13
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Pred. No. 0.0001;
0; Mismatches 69; Indels
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APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44710
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 11
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEO ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEO ID NO 13
LENGTH: 320
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                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
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Patent No. 6197510
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Best Local Similarity 58.9%;
Matches 99; Conservative
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FEATURE:

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Debussche, Laurent
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APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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Matches 133; Conserv
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-510-646B-3
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APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                     119 gggccggcggcggggggccggggcctgcaggcccccggtacgacaagatccggactccg 178
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Pred. No. 0.0043;
0; Mismatches 114; Indels
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PLICATION NUMBER: US/08/510,646B FILING DATE: 03-AuG-1995
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APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
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SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6077699
; GENERAL INFORMATION:
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Lacroix, Patricia
Thibaut, Denis
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Blanche, Francis
Crouzet, Joel
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Best Local Similarity 53.0°
Matches 133; Conservative
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OPERATING SYSTEM:
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ZIP: 20005-3315
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                             ; NAME/KEY:
; LOCATION:
US-08-403-852D-3
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APPLICANT:
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FEATURE:
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De Crecy-Lagard, Valerie
PENTION: Polypeptides Involved In The
FENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
FENTION: Coding For These Polypeptides And Their Use
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STREET: 1300 I Street, N.W., Suite 700
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53.0%; Pred. No. 0.0043;
tive 0; Mismatches 114;
NAME: MAYERS, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03806.0054-01000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000

TELEPHONE: (202) 408-4000

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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APPLICANT: Jacques, Nathalie
APPLICANT: Jacques, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy Lagard, Va
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Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
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Pred. No. 0.0058;
0; Mismatches 114; Indels 4
                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
                                                                                                                                       De Crecy-Lagard, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                              Zagorec, Monique
Debussche, Laurent
                                  Nathalie
                                                       Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.7%;
Best Local Similarity 53.0%;
Matches 133; Conservative (
Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                            Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5392 base pairs
                    Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                               APPLICANT: De Crecy-
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                       Jacques,
                                                                            Thibaut,
                                                       Lacroix,
                                                                                                                                                                                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.7%; Score 50.6; DB 4; Length 833; 53.0%; Pred. No. 0.0043; Live 0; Mismatches 114; Indels
                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REGISTRATION NUMBER: 03806.0054-00000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000

TELEPHONE: (202) 408-4000

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
TENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/403,852
FILING DATE: 10.MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                 APPLICATION NUMBER: US/09/231,818 FILING DATE:
                                                                                          PC-DOS/MS-DOS
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Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: S.pristinaespiralis
                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
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Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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US-08-403-852D-1/c
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APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent Laurent
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Goding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
                                    3418 CGGCCAGGACCGGTCGTCGGAGCCGGTGAGCCCTCAAAGCCGTCCGCGGGGCTGT 3359
                                                                                                                                                                                                                                                          3358 CGGCGGGCAGTTCGGCGGCCGGGCCGGGCAGCCAGGAGGATCTTGGCGTGCGGTGCCT 3299
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                                                                                                        63 gagec----cegggggagteggegetgetggaegggtggetgeageggggegtgggeegggg 118
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       179 goccoggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcg
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STREET: 1300 I Street, N.W., Suite 700
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APPLICATION NUMBER: US/09/231,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03806.0054-00000
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FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 92/11441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09231818 Patent No. 6171846
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jacques, Nathalie APPLICANT: Lacroix, Patricia
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Blanche, Francis
Crouzet, Joel
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-SEP-1992 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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tive 0; Mismatches 114; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-40G-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION NUMBER: PCT/FR 93/00923
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 91/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                            Sequence 1, Application US/08510646B Patent No. 6077699 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                       Debussche, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 408-4000
TELEFRAX: (202) 408-4400
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                           Lacroix, Patricia
Thibaut, Denis
Zagorec, Monique
                                                                                                                                                                                                                                                                                                                                   Jacques, Nathalie
                                                                                                                                                                                                                                                        Blanc, Veronique
Blanche, Francis
Crouzet, Joel
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MEDIUM TYPE: Floppy disk
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Matches 133; Conservative
                                                 3238 CGAGGGGGGG 3228
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CITY: Washington
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ZIP: 20005-3315
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239 ccgtggcaggg
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ORGANISM: S.p
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APPLICANT:
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APPLICANT:
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STRANDEDNESS:
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                                                                     NAME/KEY:
                                                                                       LOCATION:
                                                                                                                                        LOCATION:
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                                                                                                                                                                                                                                                                           ), NAME/KEY:
; LOCATION:
US-08-804-227C-1
                    TOPOLOGY:
                                                                                                                         NAME/KEY:
                                                                                                                                                        FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                           3418 cGCCCAGGACCGGGTCGTCGGAGCCGGTGAGCGCCACCGTGAAGCCGTCCGCGGGGGCTGT 3359
                                                                                                                                                                                                                                                                                                                                                                                                                                    3358 CGGCGGCCAGTTCGGCGGCCGGGCCGGGCAGGCAGGATCTTGGCGTGCGGTGCCT 3299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3298 GCTGCTTCACCGAGGCGGCGCGCCTCGTCGTCGAGGACGAGGACGGGGGGGCGCGGG 3239
                                                                                                                                                                                                                                                                                                                                                                                                 119 gggccggcggcggggggccgggggcctgcaggcccccggtacgacaagatccggactccg 178
                                                                                                                                                                                                                                                                                                                              63 gagcc---ccggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccggg 118
                                                                                                                                                                                                                                                             179 gcccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcg
                                                                                                                                                                                       Query Match 8.7%; Score 50.6; DB 4; Length 5392; Best Local Similarity 53.0%; Pred. No. 0.0058; Matches 133; Conservative 0; Mismatches 114; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCITOOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: FEBRUARY 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: LILLY CORPORATE CENTER CITY: INDIANAPOLIS STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08804227C Patent No. 5876991
                                                                                ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: X * 82 TELECOMUNICATION INFORMATION: TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 43280 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                  double
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3238 CGAGGGCGGG 3228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 ccgtggcaggg 249
                                linear
                              TOPOLOGY: linea
MOLECULE TYPE: CD
HYPOTHETICAL: NO
              STRANDEDNESS:
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US-08-804-227C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 cggcccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.5%; Score 49.4; DB 2; Length 43280; 50.2%; Pred. No. 0.015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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APPLICANT: KANG, Hyun-Ah
APPLICANT: KIM, Hwa-Young
TITLE OF INVENTION: AUTONOMOUSLY REPLICATING SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: RHEE, Sang-Ki
STREET: Keukdong Villa Ka-101, Kwangjang-dong,
STREET: Kwangjin-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/08903800A; Patent No. 5935789
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHEE, Sang-Ki
CHOI, Eui-Sung
KIM, Chul-Ho
                                                                                                                                                          14351..19945
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31232..36067
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36249..41774
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                                                    CDS
816..14234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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OTHER INFORMATION: autonomously replicating sequnce of OTHER INFORMATION: Hansenula polymorpha DL-1(ATCC 26012) US-08-903-800A-1
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                                                                                                                                                                                    ZIP: 305-335
ADDRESSEE: KIM, Chul-Ho
STREET: Shindonga Apt. 2-1101, Yongjeon-dong, Dong-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE KANG, Hyun-Ah
STREET: Kyungseong Keunmaul Apt. 125-1501, Kalma-dong,
STREET: Seo-gu
CITY: Daejeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: Republic of Korea
ZIP: 120-190
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKELTE, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/AT
OFFRATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,800A
FILING DATE: 31-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 97-3173
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               COUNTRY: Republic of Korea
ZIP: 300-200
ADDRESSEE: SOHN, Jung-Hoon
STREET: Nurl Apt. 103-506, Wolpyung-dong, Seo-gu
                                             ADDRESSEE: CHOI, Eui-Sung
STREET: Dasol Apt. 102-507, #395-3, Kung-dong,
STREET: Yuseong-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 302-171
ADDRESSEE: KIM, Hwa-Young
STREET: #3-462, Bukahyun-3-dong, Seodaemun-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
COUNTRY: Republic of Korea ZIP: 143-210 ADDRESSEE: CHOI, Eui-Sung
                                                                                                               CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-335
                                                                                                                                                                                                                                                                                                                                                                                                         CATATE: Daejeon
COUNTRY: Republic of Korea
7TP: 302-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1227 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      Daejeon
: Daejeon
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CITY: Seoul
STATE: Seoul
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QΩ ŏ

2; Gaps

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62 ggagccccgggggagtcggcg--ctgctggacgggtggctgcagcggggcgtgggccgggg 119
                    665 GCGGGGTGGCGGGGTGGCGGGGTGGCGTGGTCATCGGGTACAACA 709
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Search completed: September 28, 2002, 07:54:54 Job time: 11179 sec

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BI827322 603077989

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliangelifetech.com URL:
http://fullength.invitrogen.com"
83 2 4 c 132 g 139 t 15 others
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B1412175 602965377
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B1848355 64673b07.
A1942584 fc73c03.y
A1133696 Hab2320 Hu
B1831750 603201993
B1831750 603201993
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BF916224 CM2-UT011
BG712700 Mus muscu
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AKO1577 Mus muscu
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BM313240 ig8ld05.y
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 888)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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BF797743
BM313240
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AL530804
AL530804.1 GI:12794297
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282.8
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ORGANISM
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
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AL530804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
 ; Search time 4881.77 Seconds (without alignments) 1609.094 Million cell updates/sec
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BI794612 19106 MAR BI045883 MR3-FN020
AW326482 19106 MAR BR0418040 126651 MAR BE014800 MAR BE014800 126600 MAR BE014800 MAR 
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                                                                                                                                                                                                                           582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           summaries
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BG64218
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B1185580
AV704087
                                                                                - nucleic search, using sw model
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Copyright (c) 1993
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168 a

BASE COUNT

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Gaps

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/crganism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:1090"
/clone="IMAGE:5043992"
/clone="IMAGE:5043992"
/clone="IMAGE:5043992"
/clone="IMAGE:5043992"
/clone="IMAGE:5043992"
/clone="IMAGE:5043992"
/clone="IMAGE:5043992"
/clone="IMAGE:504"
/clone="Crgan: Ridney; Vector: pcMV-SPORT6; Site_1: Not1;
/cote="Crgan: Ridney: Note: This is a NCI_CGAP Library. |"
/cote="Crgan: Ridney: Ridne
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602392826F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4504638 5',
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Pred. No. 8.2e-73;
0; Mismatches 49
60
    row: 1 column:
                                               Location/Qualifiers
  Plate: LLAM11120 row: 1 cc
High quality sequence stop:
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BG295496.1 GI:13057189
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90.8%;
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nes 502; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Mustheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 817)
INH-MGC http://mgc.ndi.nh.gov/.
INH-MGC http://mgc.ndi.nh.gov/.
Insulished (1999)
I Onpublished (1999)
I Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.ih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                   240 GCCGGCSGCGGGGAGGCCGGGGCCTGCAGG-CCCCGGTACGACAAGATCCGGACTCCGGC
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                                                         91.5%; Score 532.6; DB 9 98.1%; Pred. No. 9.3e-88;
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TITLE
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Seq primer: ATTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
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1. .573
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                                         NIH WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Column: 07

High quality sequence stop: 753.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1131)
                                                                                                                                                                                                                                                                                                                                                   /cloud_lib="MIH_MGC_94"
/tissue_type="retina"
/tab_most="DH10B (phage-resistant)"
/lab_most="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cageg-ggggcgtggggccgggcggcggggggaggccggggcctgcaggccccggt 158
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91.7%; Pred. No. 1.2e-70;
live 0; Mismatches 42
                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:4504638"
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Matches 497; Conservative
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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1 (base; Lo 573)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
EST 30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
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166 c 176 g 110 t
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455541 MARC 1BOV Bos taurus cDNA 5', mRNA sequence. B1541703 E1541703.1 GI:15382815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
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Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 697)

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emall: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMIBWI row: i column: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                                                                                    taatccacctgggggcaatagccatattgccaatggtgcggccgggtgtgtggcaacat 544
                                             424
                                                                       241 TAAGAACGGAGGCCTGTGGAGGCCCATGCGAGGCCTGAACGTCACAGCAACAGGCGCAG 300
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192 c 277 g 108 t
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Pred. No. 2.3e-65;
); Mismatches 57; Indels
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/csx="female, virgin"
/tissue_type="infiltrating
/dev_stage="5 months"
/lab_host="DH108"
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/organism="Mus musculus"
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/clone="IMAGE:5387608"
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88.9%;
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BI854643
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TITLE
JOURNAL
COMMENT
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BI739710 967 bp mRNA linear EST 20-SEP-2001 603361983F1 NIH_MGC_94 Mus musculus CDNA clone IMAGE:5369084 5',
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Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 967)
NHH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepkor Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMI1939 row: e column: 21
High quality sequence stop: 677.
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                        ggggccggcggcgggggggcctgcaggccccggtacgacaagatccggactcc
                                                                                                                                                242 GGGGCCGGCGGGGGGGGGGCGCCTATCAGCCCCTGTACGGCTGGATCCGGAGTCC
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                                                                                                                                                                                                                                302 GGCCCGGAATACGAAGCGCTGCCGGCTGGAGCCACTGTCACCACCACATGGTGGCGGGC
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/clone="IMAGE:5369084"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
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    967
    /organism="Mus musculus"

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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Inoyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602828996F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983815 5', mRNA sequence.
BG964218
BG964218.1 GI:14351855
EST.
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/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                         410 GATGCAGAGCCTACAGCCTGACCCAGCCGCCGCTATCGGAACGTTGGAGGCTCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            aggogagaggoctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacatt
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9
                                                                                                       Length 967;
                                                                                                                               Indels
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                                                                                                      DB 10;
                                                                                                                              48;
                                                                                                      Score 398.2; DB 1
Pred. No. 2.9e-63;
0; Mismatches 48
                                                                                                       68.4%;
89.8%;
                                                                                                                          473; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                      Query Match
Best Local Similarity
Matches 473; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
                                                         154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                         BASE COUNT
                                                                                                                                                                                              61
                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                  231
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TITLE
JOURNAL
COMMENT
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BG964218
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EST 09-JUL-2000
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Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 cggggaggccggggcctgcaggcccccggtacgacaagatccggactccggcccggacta 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 ACAGCCTGACCCAGCCGCCCGCTATCGGAACGTGTTGGAGGCTCTCTGGAGAATCATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 bp mRNA linear
BE012485
BE012485.1 GI:8273406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM1098B row: p column: 24
High quality sequence start: 2
High quality sequence stop: 632.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.5%; Score 387; DB 10; Best Local Similarity 91.1%; Pred. No. 3.2e-61; Matches 411; Conservative 0; Mismatches 40;
                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 tcatgatgcagccatgaaccctgcggaaggc 579
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Best Local Similarity 94.6
Matches 388; Conservative
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    ORGANISM
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                                                  USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAAACAGCTATCACCAT
BACKWARD: GTTTTCCCAGTCACACAT
BACKWARD: GTTTTCCAGTCACACATAG.
Seq primer: ATTTAGGTGACATAAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNL-P-FN-cy-f-02-0-UNL.S1 UNL-P-FN Sus scrofa cDNA clone UNL-P-FN-cy-f-02-0-UNL.31 UNL-P-FN Sus scrofa cDNA clone UNL-P-FN-cy-f-02-0-UNL 3', mRNA sequence. B1185580.1 G1:14659989 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
 pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embruce "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 acaagatccggactccggcccggactacgagcgctgccggctggagccactgtcaccac 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcacatggtggcaggcgcgtggcagggatcctggagcactgcgtgatgtacccatcga 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 gttggaggccctctggaggattataagaacggaggcctatggaggcccatgaggggct 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 gcggggcgtgggccggggggccggcggcggggggggccgggcctgcaggcccccggtacg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GCACATGGTGGCGGCGCCGTGGAAGGAATCCTGGAGCACTGGGTGATGTACCCCATCGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GCGGGGCGTGGGCCGGGGGGCCGGGGGGCCGGGGCCTGCAGGCCCCCGGTAAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 367.2; DB 9;
Pred. No. 1.3e-57;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                       /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        141 g
                                                                                                                                                                                                                                                                                                                                                                             and 30 embryos
           EST discovery in swine Unpublished (2000)
Design and use of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                63.18;
95.58;
                                                                                                                                                                                                                                                                                                                                                                                         117 c
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.1
Best Local Similarity 95.5
Matches 378; Conservative
                                                                                                                                                                                                                                                       1. .397
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VERSION
KEYWORDS
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                         JOURNAL
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Julies "UNL-P-FN-cy-f-02-0-UNL" / Clone="UNL-P-FN-cy-f-02-0-UNL" / Clone="UNL-P-FN-cy-f-02-0-UNL" / Clone="UNL-P-FN" / Clone="UNL-P-FN" / Clone="UNL-P-FN" / Clone="UNL-P-FN" / Clone="UNL-P-FN" / Clone="Vector: pT73D-pec (Pharmacia) with a modified / Note="Vector: pT73D-pec (Pharmacia) with a modified polylinker; Site=1: Not I: Site=2: Eco RJ: The UNL-P-FN library is a normalized library representing porcine ovarian follicles, ranging between 2: 0 to 10.0 mm in diameter, collected during 7 between 2: 0 to 10.0 mm in diameter, collected during 7 a string of 5-6 incleotides present between the Not I site and the nucleotides present between the Not I site and the oligo-dr track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
Eukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

CE 1 (bases 1 to 574)

RS Caetano,A.R., Johnson,R.K. and Pomp,D.
Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles
Upublished (2001)
Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6416
Email: dopm@buil.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
/strain="University of Nebraska, Lincoln Swine Selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 ccggactccggacccggactacgaggcgctgccgg-ctggagccactgtcaccacgcacat 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caagacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttgga 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggccctctggaggattataagaacggaggcctatggaggcccatgagggggctgaacgt 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cacagcaacaggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaa 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 354.6; DB 10; Leuser.
Pred. No. 2.6e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligo-dr track. The library wa by Bonaldo, Lennon and Soares, , 1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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171 c 165 g
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94.6%;
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BE913718 598 bp mRNA linear EST 29-SEP-2000 601669072F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3969256 5',
                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9146 row: o column: 17
High quality sequence stop: 593.
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                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 598)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/dev_stage="10 months, virgin"
/lab_host="DH10B"
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Pred. No. 1.5e-53;
0; Mismatches 25;
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/organism="Mus musculus"
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/clone="IMAGE:3969256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="FVB/N"
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93.5%;
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Matches 360; Conservative
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                                                                                                             mRNA sequence.
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Homo sapiens cDNA ADB clones
L Unpublished (2000)
Contact: Zeguang Han Genome Center at Shanghai
Sin Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex. 45)
Fax: 86-21-50801922
Email: hanz@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 681)
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Pred. No. 8.1e-54;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="ADB"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADBAFE05"
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Matches 347; Conservative
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Length Indels 454

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Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=MR3&t2=MR3-FN0209-300101-004+hl0&t3=2001-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 480.
Location/Qualifiers
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1 (bases I to 480)

1 bases I to 480.

1 dases I to 480.

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI045863 480 bp mRNA linear EST 14-JUN-2001 MR3-FN0209-300101-004-h10 FN0209 Homo sapiens CDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                              455 acgaaaagttaaaaaagacattgagtgatgtaatccaccctgggggcaatagccatattg 514
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                            DB 10;
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Pred. No. 1.3
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92.9%;
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                                                                         Query Match 55.6
Best Local Similarity 92.9
Matches 339; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E l'bases I to 560)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Endocrine Pancreas Consortium
L. Unpublished (2000)
Other_EsTs: ic92e02.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA, 02138
                                                                                                                                                                                                                               BI794616 560 bp mRNA linear EST 01-OCT-2001 ic92e02.yl Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus cDNA 5' similar to TR:Q23125 Q23125 W02B12.9 PROTEIN. [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: dmelton@blobp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adult islet"
/dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,
adult, mixed"
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301 AGGGGGCAATAGCCATATTGCCAATGGTGCAGCCGGATGTGTGGCGACATTACTTCATGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone_lib="Melton Normalized Mixed Mouse Pancreas 1
N1-MMS1"
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/organism="Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (brown@fas.harvard.edu)
                                            555 tgcagccatgaacctgcggaaggc 579
                                                                                                 361 TGCAGCCATGAATCCAGCGGAAGTC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                ;, mkNA sequence.
BI794616
BI794616.1 GI:15822341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                              Score 302.2; DB 9;
Pred. No. 9.4e-46;
0; Mismatches 13;
                                                                                                                                                                                        /db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
Plate: 8 row: F column: 16
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                           /organism="Bos taurus"
                                                                                                                                            Location/Qualifiers
                                                                      FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caatggtgcggccgggtgtgtgg 538
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96.0%;
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Matches 310;
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BM488747
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AUTHORS
TITLE
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                     puc18; Site_1: Smal
                                                                                                                                                                                                                                                                                                                       ij
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         /organism="Homo sapiens"

/db_xref="taxon:9606"

/db_xref="Taxon:9606"

/dclone_lib="FN0209"

/dev_stage="Adult"

/note="Organ: prostate_normal; Vector: pucl8; Site_1: Sma; Site_2: Smal; A mini-library was made by cloning

/ Site_2: Smal; A mini-library was made by cloning

/products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 GTCACAGCAACAGGGCCTGCCCACGCGCTTTATTTTGCCTGCTACGAAAAGTTA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                              286 gicaagacccggaigcagagictacagcctgacccagcigcccgciaicgcaaigigiig 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 gtcacagcaacaggcgcagggcctgcccacgccctttattttgcctgctacgaaaagtta 465
                                                                                                                                                                                                                                                                                                                                                       226 atggtggcaggcgccgtggcagggatcctggagcactgcgtgatgtaccccatcgactgc 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AAAAAGACATTGAGTGATGTAATCCACCCTGGGGGGCAATAGCCATATTGCCAATGGTGC 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                          performed under low stringency conditions." 126\ c 146\ g 92\ t
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                                                                                                                                                                                                                                                                   Score 320.2; DB 10; Lews-
Pred. No. 4.9e-49;
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19106 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW326482
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                55.0%;
96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pitultary."
                                                                                                                                                                                                                                                                                                                                                                                                                                            caccacgcacatggtggcaggcgccgtggcagggatcctggagcactgcgtgatgtaccc 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 546)
Cogburni.A. and Monsonego-Ornan,E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgaaaaagttaaaaaagacattgagtgatgtaatccaccctgggggcaatagccatattgc 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAAAGTTAAAAAAGACATTGAGTGATGTAATCCACCCTGGGGGCAATAGCCATATTGC 313
                                                                                                                                                                                                                                                                                                                                                                ggggctgaacgtcacagcaacaggcgcagggcctgcccacgccctttattttgcctgcta
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus,
                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                           Length 336;
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/dev_crepte="Breast,leg:Embryo(d19):post-hatch(ld,1,3,5,7,9,11 weeks):growth plate(ld,7d,14d post-hatch)"
/ll weeks):growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B."
/note="vector: pcMvSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic mascle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       j;
                                                                                                                                                                              /db_xref="taxon:9031"
/clone="pgm2n.pk008.12"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="wale and Female"
/tissue_type="Breast muscle, leg muscle and epiphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 taccccatcgactgcgtcaagacccggatgcagagtctacagcctgacccagctgcccgc 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                         Ottawa Res. Centre
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Pred. No. 4.6e-45;
0; Mismatches 109; Indels
                                          Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburneddel.edu, www.chickest.udel.edu.
Location/Qualifiers
                                                                                                                                      /organism-"Gallus gallus"
/strain-"Commercial broiler and
Strains 90 & 21"
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                Contact: Larry A. Cogburn
University of Delaware
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77.0%;
Unpublished (2002)
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Search completed: September 28, 2002, 06:22:39 Job time: 9180 sec

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Title: Perfect score:

Sequence:

OM nucleic

on:

Run

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Aj303077 Homo sapi
Aj303078 Homo sapi
AX061229 Sequence
AL53719 Human DNA
AX071440 Sequence
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AX0736189 Mus muscu
AF223466 Homo sapi
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AC015028 Sequence
Z66521 Caenorthabdi
AX060268 Drosophil
AY000268 Drosophil
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AX10628 Sequence
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AC098461 Rattus no
AC097177 Rattus no
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Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R., Larsson,C. and Suomalainen,A.
Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing
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FEBS Lett. 494 (1-2), 79-84 (2001)
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AP003518
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                                                     ; Search time 5287.54 Seconds
(without alignments)
2742.691 Million cell updates/sec
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      version 4.5
- 2000 Compugen Ltd.
                                                                                                                                              1797656 seqs, 10463268293 residues
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Maximum Match 100%
Listing first 45 summaries
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      GenCore
Copyright (c) 1993
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em_htg_hum:*
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and is derived by analysis of
                                                                                                                                                                              seq length: 0 seq length: 2000000000
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(bases 1 to 1448)

11297739

Description

Score

Result

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Sequence 1448
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26-APR-2001
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LQDPDAARYRNVLEALWRITRTEGIWRPMRGLNVTATGAGPAHALYFACYEKILKTLLS
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Li,F., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R. Larsson,C. and Suomalainen,A. Direct Submission
Submitted (08-DEC-2000) Human Molecular Genetics, National Public Health Institute, Mennerhalmintle 166, Helsinki 00300, Finland Location/Qualifiers
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                                                                                                                                /product="putative mitochondrial solute carrier splice variant"
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/chromosome="10"
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100.0%; Pre
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AFYRSYTTGLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTP
LDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTA
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/function="putative mitochondrial solute carrier"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-DEC-2000) to the EMBL/GenBank/DDBJ databases.
Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Larsson C., Suomalainen A.;
Larsson C., Suomalainen A.;
"Characterization of a novel human putative mitochondrial transporter
homologous to the yeast mitochondrial RNA splicing proteins 3 and 4";
FEBS Lett. 494:79-84(2001).
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llarity 100.0%; Pred. No. 2.6e-88;
Conservative 0; Mismatches 0;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
          NTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAMSVYE
FFKYLITKRQEEWRAGK"
508 c 544 q 433 t
LIMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLL
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                                                                                                                                                                                                                                         Score 520.4; DB 9; Length 1889;
Pred. No. 9.4e-79;
0; Mismatches 1; Indels 0;
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26-APR-2001 (Rel. 67, Last updated, Version 2)
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/db_xref="G1:13926050"
/translation="MNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQ
                                                                                                                                                                                                                                                                                                                                                                                       PRI 02-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li.F., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R. Larsson,C. and Suomalainen,A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-DEC-2000) Human Molecular Genetics, National Public Health Institute, Mennerheimintle 166, Helsinki 00300, Finland Location/Qualifiers
1. .1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1889)
Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B.,
Schweyen,R., Larsson,C. and Suomalainen,A.
Characterization of a novel human putative mitochondrial
transporter homologous to the yeast mitochondrial RNA splicing
proteins 3 and 4
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/db_xref="taxon:9606"
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/codon_start=1
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/map="10q24"
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protein 3/4 (HMRS3/4

Bandman, O.,

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Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 123160)
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                                                                                                                          ., Hillman,J.L., Tang,Y.T., Bandman,
., Azimzai,Y., Lu,D.A., Au-Young,J.
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/db_xref="taxon:9606"
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Primates;
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Burford,N., Baughn,M.R.,
Patterson,C.
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Patent: WO 0078953-A 76 2
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Mammalia, Eutheria, P
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/protein_id="CAC27997.1"
/protein_id="MNPAVVQRMOMYNSPYHRVTDCVRAVWQNEGGGAFYRSYTTQL
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QESLALNSHITGHITGMASAFRTVXQVGGVTAYFRCVQARVIYQIPSTAIAWSVYEFFR
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Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
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                                                         Li F., Nikali K., Gregan J., Leibiger I., Leibiger B., Schweyen R., Larsson C., Suomalainen A.; "Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing proteins 3 and 4";
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/db_xref="taxon:9606"
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/gene="HMRS3/4"
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                                                                                                                        FEBS Lett. 494:79-84(2001).
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REFERENCE AUTHORS

PAT 22-JAN-2001

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Rattus norvegicus
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                                                               requests: clonerequest@sanger.ac.uk
On Sep 26, 2001 this sequence version replaced gi:14280413.
During sequence assembly data is compared from overlapping clones.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with regions were correct outly as the corresponding to the overlapping clone, as we submit sequences with only a small overlap as described as follows unless otherwise noted: all regions were covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw.; SWISSRROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP that the continue table with their source databases: Em: EMBL; Sw.; SWISSRROT; Tr.; TREMBL; Wp.; MORMPEP; Information on the WORMPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/HGP/Chrl0
RP11-85A1 is from the library RPCI-11.1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
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The true left end of clone RPI1-85A1 is at 1 in this sequence. The true left end of clone RPI1-83811 is at 123061 in this sequence. The true right end of clone RPI1-129512 is at 51589 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGGCGGCGGGGGCCCGGGCCTGCAGGCCCCCGGTACGACAAGATCCGGACTCCGGC 91778
                      Submitted (25-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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//note="Single clone region. Sequence from reads from a short insert library derived from a single puC clone. Restriction digest data confirm the assembly."
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AC096351 221062 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus chromosome Rf1 clone CH230-24M6, WORKING DRAFT
SEQUENCE, 33 unordered pieces.
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Patent: WO 0102568-A 1912 11-JAN 2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Length 401;
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100.0%; Pred. No. 7.6e-37;
rive 0; Mismatches 0;
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/db_xref="taxon:9606"
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104 c 120 g
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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AX071440.1 GI:12581791
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/organism="Rattus norvegicus"

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RS Muzny, D.M. Addama, C., Adio-Oduola, B., Ali-osman, F. R., Allen, C., Alabrooks S. L., Amaretunge, H. C., Are, J. R., Banks, T., Barbaria, J., Babrooks, S. L., Amaretunge, H. C., Are, J. R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burkett, C., Burrell, K.L., Byrd, N. C., Carron, T. F., Carter, M. Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Dederich, D., Dalaney, K.R., Delgado, C., David, R., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Denn, A.L., Ding, Y., Dinh, H. H., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C. C., Elbaj, C., Escotto, M., Ealls, T., Ferraguco, D., Elagar, D., Edwards, C., Elbaj, C., Escotto, M., Salls, T., Earnhart, C., Edgar, D., Edward, J., Hamilton, K., Harris, C., Harris, R., Harris, M., Gulla, R., Garcia, A., Garner, T., Garza, M., Gillin, R., Gorrell, J. H., Guevara, W., Gunzarene, P., Hamilton, K., Harris, C., Harris, R., Harris, R., Harris, R., Harris, R., Harris, C., Harris, R., Howard, S., Karlsson, E., Jacchson, B., Jackson, R., Jackson, R., Jackson, R., Jackson, R., Jackson, R., Lui, T., Li, Z., Lintharge, C., Lieu, Y., Males, H., Lozado, R.J., Lu, X., Lucier, R., Lucier, R., Luna, R., Mattinez, B., Massey, E., Mawhiney, E., Martin, R., Massey, E., Mawhiney, E., Martin, R., Massey, E., Mawhiney, E., Martin, R., Massey, R., Perez, L., Peters, L., Pickers, R., Peters, R., Pathons, N., Niyyen, N., Sisson, I., Sodergen, E.,
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NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is
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Consensus quality: 205303 bases at least Q30
Consensus quality: 209366 bases at least Q30
Estimated insert size: 209880; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
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Contact: hgsc-help@bcm.tmc.edu
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/db_xref="taxon:10116"
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Peery, J., Perez, L., Petchers, R., Primus, E., Pu, L.L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
Tang, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, R.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
Mall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,
Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15627972.
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Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hqsc.bcm.tmc.edu/
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Center project name: GEZD
Center clone name: CH230-24M6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Center
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Direct Submission
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PLRGLNVMMMGAGPAHAMYFACYENMKRTLNDVFSHQGNSHLANGVAGSMATLLHDAV MYMPADVYGRLDMYNSHQARSTRTOLTNHFPGSHFTTY YEFLGEGVNPRRDYRPGSHT I SGGLAGALARATPLDVCKTLLNTQBNMALGLANVS GRLSGMANAFRTVYQLNGLAGYFKGIQARVIYQMPSTAISWSVYEFFKYILTKRQLEN
                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MELRRGGVGNQAAGRRMDGDCRDGGCGSKDAGSEDYENLPTSAS VSTHWTAGAMAGILEHSIMYPVDSVKTRMQSLNPDPKARYTSIYGALKRIMHTEGFWR
         Mus musculus mitochondrial solute carrier-like protein mRNA, complete cds.
                                                                                                                           1 (bases 1 to 4112)
Li,Q.-Z., Ruan,Q.-G., Eckenrode,S., Shi,J.-D., Cruz,P., Wang,C.-Y. and She,J.-X.
                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                          Submitted (20-JUL-2000) Pathology, University of Florida, 1600 Archer Road, Rm. D6-15, Gainesville, FL 32610, USA Location/Qualifiers
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/product="mitronondrial solute carrier-like protein"
/protein_id="AAL23859.1"
/db_xref="G1:16506178"
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                                                                                                                                                                 A new gene which is highly expressed in NOD mice spleen
Unpublished
                                                                                                                                                                                                        2 (bases 1 to 4112)
LilQ.-Z., Shi,J.-D., Cruz,P., Echenrode,S., Ruan,Q.-G.
Wang,C.-X.
Direct Submission
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Pred. No. 8.1e-26;
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/organism="Mus musculus"
/db_xref="taxon:10090"
116. .1132
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Local Similarity 64.4%;
les 327; Conservative (
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/chromosome="Rf1"
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goccacgocotttattttgcctgctacgaaaagttaaaaagacattgagtgatgtaatc 489

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GATGGCCGGGATCCTGGAGCACTCGGTCATGTACCCGGTGGACTCGGTGAAGACACGAAT
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vsthwtagamagilehsvmypvdsvktrmqslspdpkaqytsiygalkkimrtegfwr
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yerloevynphrtymoshiisgglrgalaatataldvcktillnjonvalslanis
grlsgmanaprtyyqlnglpatskasrrysstrcppppflglsmsssstfspsaswki
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1429)
                                                                                                                                                                                                                                                                                                                                                                                                 Song, H., Gao, G., Peng, Y., Ren, S., Chen, Z. and Han, Z.
Direct Submission
Submitted (12-JAN-2000) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai Location/Qualifiers
1. 1429
                                            cggagccccgggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccggggg 120
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GCGCACGCCATGTATTTGCCTGCTATGAAACATGAAAGGACTTTAAATGACGTTTTC
                              23 CTGCGCCCGAGCTGGCGATGGAGCTGCGCAGCGGGAGCGTGGGCAGCCAGGCGGT
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Homo sapiens HT015 protein (HT015) mRNA, complete cds.
AF223466
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/db_xref="taxon:9606"
/tissue_type="hypothalamus"
1. .1429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="HT015 protein"
/protein_id="AAF64141.1"
/db_xref="G1:7578783"
                                                                                                     catgatgcagccatgaacctgcggaag 577
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/evidence-not_experimental
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/db_xref="G1:16755528"
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PLRGLNVWMGAGPAHAMYPPCYENWKRTLNDVFSHQGNSHLANGILKAFVWSWEALL
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SW Archer Road,
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                                                                                                                                                                           gattataagaacggaggcctatggaggcccatgagggggctgaacgtcacagcaacagg
                                                                                                              gcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctggag
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                             577
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Pred. No. 7.3e-21;
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/strain="C57BL/6J"
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1427 c 1390 g 16
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Strausberg, R.
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Matches 289; Conserv
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Li,Q.-Z., Eckenrode,S., Ruan,Q.-G., Wang,C.-Y., Shi,J.-D., McIndoe,R.A. and She,J.-X.
Molecular cloning of a novel microchondria solute carrier protein (MSCP) gene from mouse and human and its down-regulation in mouse spleen during the maturation of the immune system
                                                                                                                                                             489
                                                                                                                    249
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                                                                     133 gaggccggggcctgcaggcccccggtacgacaagatccggactccggccc---ggactac 189
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                                             GCGGGGCCGCGGATGGAGCTCCGCCGTGGCGCTGGGGAACCAGGCTGCGGGCCGGAGG 163
  Gaps
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                                                                                    cagoctgacccagotgcccgctatcgcaatgtgttggaggccctctggaggattataaga
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                                                                                                                    gaggcgctgccgctgtcaccacgcacatgtggcaggcgccgtggcaggg
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L1,O.-Z., Eckenrode,S., Ruan,Q.-G., Wang,C.-Y., Shi,J.-D.
McIndoe,R.A. and She,J.-X.
Direct Submission
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-APR-2001) Department of Pathology, Laboratory Sciences, University of Florida, 1600 Room D6-15, Gainesville, Florida 32610, USA Location/Qualifiers
 162;
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/note="alternatively spliced"
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             556
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/db_xref="taxon:9606"
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/product="mitochondria solute carrier protein"
/ppotein_id="AAK$154.1"
/db.xref="G1:13774109"
/translation="MELRSGSVGSQAVARRMDGDSRDGGGKDATGSEDYENLPTSAS
YETHWAGAAAAGILEHSVMYPVDSVKTRMQSLSPDPKAQYTSIYGALKKIMRTEGFWR
PLRGVNVMINGAGPAHAMTRACYENMKRTLNDVFHHQGNSHLANGILKAFVWS"
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Submitted (01-007-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419
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DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                      Length 3415;
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Catarrhini; Hominidae;
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IMAGE:3910567, mRNA,
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                                                                                                                                                                                                                                                                      Score 174.2; DB 9;
Pred. No. 3.1e-20;
); Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgatgtaatccacctgggggcaatagccatattgccaatggt
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Mammalia; Eutheria; Primates;
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BC015013
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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62.4%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MELRSGSVGSQAVARRWDGDSRDGGGGRDATGSEDYENLPTSAS VSTHWTAGAMAGILEHSVMYPVDSVKTRMQSLSPDPKAQYTSIYGALKKIMRFEGFWR PLRGVNVWIMGAGPAHAMYFACYENWKRTLNDVFHHQGNSHLANGILKAFVWS" 220 c 231 g 192 t
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Rattus norvegicus clone CH230-84G11, *** SEQUENCING IN PROGRESS
***, 71 unordered pieces.
                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                               through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 15 Row: h Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7706149.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 GAGTTTGAGTCCCAGATCCCAAAGCCCAGTACACAAGTATCTACGGAGCCCTCAAGAAAT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NHLMGC_71"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/clone="MGC:8764 IMAGE:3910567"
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69.1%; Pred. No. 8.5e-20;
iive 0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAH15013.7
/db_xref="GI:15929110"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 127058 bases at least Q40 Consensus quality: 138264 bases at least Q30 Consensus quality: 146548 bases at least Q20 Estimated insert size: 120308; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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------- Project Information
Center project name: GH131
Center clone name: CH230-84G11
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           Note: This is a working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2000
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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COLUMNICO	Query	Match Length DB ID Description	1336 21 AAC90457	66.1 1418 21 AAC74843 Human ORFX ORF398	1322 22 AAF27733	1294 22 AAI60661	2502 22 AAS03906	1316 22 AAI58875	401 22 AAF66156	27960 22 AAK69779	
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(HUMA-) HUMAN GENOME SCI INC

polyn mitoc bone immun full-	Human CDNA CLONE r Human OKFX ORF2730 Human Dolynucleoti Human cDNA 5'-end Human CDNA 5'-end Human DONE CLONE r	Human secreted pro Human secreted pro Human onerx oner2144 Human gene express Human gene express Human immune/haema Mouse ischaemic co Aspergillus oryzae Drosophila melanog	Human ımmune/haema Human ORFX ORF2729 Human OOLON Cancer Human polynuclecti Primer used in the Primer used in the Human ovarian tumo Human II-lar BAC CDNA sequence #574	Primer used in the DNA encoding novel DNA encoding novel DNA encoding novel Primer used in the Mouse ischaemic co
AAK52172 AAF59920 AAH90057 AAK58672 AAK94897 AAK92357	AAK93895 AAK94871 AAC97175 AAK91764 AAK93200 AAH89944	AAV84573 ABA83356 AAC77189 AAZ13026 AAX15876 AAK80493 ABI99871 ABI98627	AAK83876 AAC07174 AAAC0264 AAI84504 AAA38186 AAX17506 AAX02974 AAX62787	AAS84408 AAS84408 AAS76210 AAA38183 AB199656
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ALIGNMENTS

RESULT

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Human; uncoupling protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; neuroprotective, antibacterial; opthalmological; gastrointestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; gene therapy; cancer; wound; infectious disease; thrombosis; arthritis; infertility; ss.
             BP.
                                                                                   Human uncoupling protein cDNA #6
            AAC90457 standard; cDNA; 1336
                                                                                                                                                                                                                                                                                       99US-0128701.
99US-0142821.
99US-0149448.
99US-0164751.
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                                                           12-MAR-2001 (first entry)
                                                                                                                                                                                                                   WO200061614-A2.
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08-JUL-1999;
18-AUG-1999;
12-NOV-1999;
                                                                                                                                                                                              Homo sapiens
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                                     AAC90457;
AAC90457
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                                                                                                                                                                                                                  encoding uncoupling proteins. The nucleotide sequences may be used for
the detection of various disorders such as cancer, for chromosome
identification, as chromosome markers and for numerous other diagnostic
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vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                    or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
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                                                                                        Uncoupling proteins and nucleic acid sequences encoding them, usefu. for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders -
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Pred. No. 3.4e-91;
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 1336 BP; 333 A; 377 C; 358 G; 268 T; 0 other;
   Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                               Claim 1; Page 306-307; 343pp; English.
 Ni J, Komatsoulis G,
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99.88;
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                                   2000-656322/63
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatoropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic upus retrieved the analysis of immunodeficiency (SCID), AIDS, viral, bacterial or tungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, noctural haemolophintia, antinflammatory disease; to enhance
                                                                                                     hypertension;
anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; immunostive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autofimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
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100.0%; Pred. No. 9.3e-89;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 853-854; 5507pp; English.
                                                                                                                                                                                                                                                                 thrombosis; contraceptive; ss
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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Matches 458; Conserv
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                                                                                                                                                                                                                                                                                                    oort protein; TPPT; transport disorder; metabolic disorder;
disorder; cardiovascular disorder; reproductive disorder;
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Patterson
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Lu DAM, Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 160; 165pp; English.
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99US-0149357.
99US-0162287.
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immune disorder; cancer; ss
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                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-041424/05.
                                                                                                                                                                                                                                                                                                    Human; transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB60113
                                                                                                                                                                                                                                                                                                                                                  WO200078953-A2
                                                                                                                                                                                                                                                                                                                                                                                16-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-1999;
18-AUG-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                    28-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1999;
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                            ccgggggggcggcggcggggggggggggcctgcaggcccccggtacgacaagatccgga 173
                                                                                                                                                                                                 ccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccct 353
                                                                                                                                                                                                                                                                                                                                                                       ctggaggattataagaacggaggcctatggaggcccatgagggggggtgaacgtcacagc 413
                                                                                                                                                                                                                                                                                                                                                                                                                                              aacaggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaagac 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attgagtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtg 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                cggggggccggcggcgggggggggggcctgcaggccccggtacgacaagatccgga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aggogocgtggcagggatcotggagcactgcgtgatgtacoccatcgactgcgtcaagac
                                                                                         ;
0
                                                       22; Length 1322;
                                                                                         Indels
T; 0 other;
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                                                     Score 454.4; DB 22;
Pred. No. 5.4e-88;
; Mismatches 6;
267
 .;
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 4650.
C; 351
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AAI60661/c
ID AAI60661 standard; CDNA; 1294
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2000US-0620312.
2000US-0653450.
2000US-0662191.
BP; 328 A; 376
                                                   55.6%;
Similarity 98.7%;
Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US34263
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2000US-0552317.
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Sequence 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000;
                                                                      Local Simi
hes 458;
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                                                     Query Match
Best Local S
Matches 458
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protein; autoimmune disorder; hyperproliferative disorder;

(first entry)

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cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; bacterial infection; viral infection; ss; fugal infection; coular disorder; wound healing; tissue regeneration; epithelial cell proliferation; skin ageing; chemotaxis; IgG Pc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Komatsoulis G, Ruben SM, Rosen CA;
                                            AAS03906 standard; cDNA; 2502 BP.
                                                                                                                                    Human secreted protein gene #25.
                                                                                                                                                                                                                                                                                                                                               26-SEP-2000; 2000WO-US26324.
                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                   Human secreted
                                                                                                                                                                                                                                                                                     WO200123598-A1
                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                          27-SEP-1999;
                                                                                                       29-AUG-2001
                                                                                                                                                                                                                                                                                                                 05-APR-2001
                                                                          AAS03906;
                              AAS03906
                                                            ö
                                                                                                                                                                                                                                                                               Immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system closalised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scereosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such collamorate containing and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                    ombolytic activity, cancer diagnosis and therapy, drug screening, for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed
                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1294 CGGGGCCTGCAGGCCCCCGGTACGACAAGATCCGGACTCCGGCCCGGACTACGAGGCGCT 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1234 GCCGGCTGGAGCCACTGTCACCACGCACATGGTGGCAGGCGCCGTGGCAGGGATCCTGGA 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 cggggcctgcaggccccggtacgacaagatccggactccggcccggactacgaggcgct 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 gccggctggagccactgtcaccacgcacatggtggcaggcgccgtggcagggatcctgga 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cccagctgcccgctatcgcaatgtgttggaggccctctggaggattataaagaacggaggg 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cctatggaggcccatgagggggttgaacgtcacagcaacaggcgcagggcctgcccacgc 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                                       The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 gcactgcgtgatgtaccccatcgactgcgtcaagacccggatgcagagtctacagcctga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cctttattttgcctgctacgaaagttaaaaagacattgagtgatgtaatccaccctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1054 CCTATGGAGGCCCATGAGGGGGCTGAACGTCACAGCAACAGGCGCAGGGCCTGCCCACGC
                                                                        Ren F, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%; Score 440; DB 22; Length 1294;
100.0%; Pred. No. 6.4e-85;
live 0; Mismatches 0; Indels 0;
                                                                        Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1294 BP; 267 A; 335 C; 368 G; 324 T; 0 other;
                                                                        ku C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                        Claim 1; SEQ ID NO 4650; 10078pp; English.
                                                                          Chen R,
                                                                                         χα c,
                                                                       Liu C, Asundi V, Che
Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440; Conservative
                                                                                                                                 WPI; 2001-442253/47.
P-PSDB; AAM41505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                   assays for recept
C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification.
                                                                                      Wang J, W
Zhao QA,
                                                                       YT,
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Sequences AAS03873-AAS03922 represent isolated nucleic acid molecules and PCR primers of the invention. acid of the invention. Secreted proteins and their related nucleic acids can be used in the diagnosis of or susceptibility to a pathological condition by determining the presence or absence of a mutation in a nucleic acid or the presence or amount of expression of a secreted protein. The sequences are used to prevent treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The antibodies to the polypeptides can also be used in alleviating symptoms associated with disorders and in diagnostic immunosasys e.g. radioimmunosasys or enzyme linked immunosorbent assays (ELISA). The disorders include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. carbotast, cerebrovascular disorders e.g. carbotast isolamena, anajogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infections to mainteen the mainteent of the connect of 
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                                                                                                                                                                                        Forty one nucleic acid molecules encoding human secreted proteins, usef in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 gtgggccggggggccggcgggggggggggccgggcctgcaggcccccggtacgacaagat 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 ccggactccggcccggactacgaggcgctgccggctggagccactgtcaccacgcacatg 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 gtgggccggggggccggcggcggggggggccgggggcctgcagg-cccnggtacgacaagat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 460-461; 518pp; English.
WPI; 2001-281684/29.
P-PSDB; AAU01950, AAU01989.
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les 412; Conservative
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498

934 GGGCAATAGCCATATTGCCAATGGTGCGGCCGGGTGTGTGCGCAACATTACTTCATGATGC

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577
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                                                                                                                                                     Query Match 57.5%;
Best Local Similarity 95.5%;
Matches 421; Conservative
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                                                                                                             specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF66156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
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                                                      348
468
                                                                                                                                     365
                                       gtggcaggcgccgtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtc 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating disorders
                       aagacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggag
                                                              acagcaacaggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaa
                                                                                                                                     acagcaacaggcgcagggcctgcccacgccctttatttgcctgctacgaaagttaaaa
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Zhang J;
                                                                                                                                                    Qian XB,
Yang Y,
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Ku C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1078; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as central nervous system injuries
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                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Asundi V, Che
Pang Z, Wehrman T, Xu
Zhou P, Goodrich R,
                                                                                                                                                                                                             AAI58875 standard; cDNA; 1316
                                                                                                                                                                                                                                                                                                                                                                                               2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0727344
                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                WO200153312-A1.
                                                                                                                                                                                                                                                                                                                   leukaemia; ss
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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03-AUG-2000;
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09-JUL-2000;
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Wang J, Y
                                                                                                                                                                                                                            AAI58875;
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                immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as alzeheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Draqer Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, chemotactic/chemokinetic activity, democratic/chemokinetic activity, democratic/chemokinetic activity, and thrombolytic activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                      C.N.5 disorders. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 cggggcctgcaggcccccggtacgacaagatccggactccggcccggactacgaggcgct 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded polypeptides (AAM38642-AAM42213) with nootropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1316 BP; 335 A; 364 C; 337 G; 280 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 398.6; DB 22;
Pred. No. 4.4e-76;
0; Mismatches 19; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; gene therapy; colon cancer; cancer; lung cancer; cancer detection; s
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(CHIR) CHIRON CORP. (HYSE-) HYSEQ INC.

02-JUL-1999; 02-JUL-1999;

11-JAN-2001

Williams LT,

WPI; 2001-091805/10.

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24591
                                                                                                                                                                                                                                                                                                             2000US-0205515.
2000US-0209467.
2000US-0214886.
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2000US-0216647.
2000US-0216880.
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2000US-0220963.
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2000US-0224519.
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2000US-0231243
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06-NOV-2001 (first entry)
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                                                                                                                          WO200157182-A2
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17-MAR-2000;
18-APR-2000;
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07-JUN-2000;
28-JUN-2000;
                                                                                                 Homo sapiens
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14-AUG-2000;
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22-AUG-2000;
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                                                                                                                                                      09-AUG-2001
The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or Lissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
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                                                                                                                                      ), Klinger J, Kassam A;
Lamson G, Drmanac R;
Leshkowitiz D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425 ggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattgagtgatg 484
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Dickson M, Labat I,
LW, Strache-Crain B;
                                                                                                                                         Garcia PD,
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                         30-JUN-2000; 2000WO-US18374
                                                     99US-0142310
                                                                 99US-0142311
                                                                                                                                                   Reinhard C, Randazzo F,
Crkenjakov R, Drmanac S,
Kita D, Garcia V, Jones
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Best Local Similarity Matches 273; Conserv

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Query Match

2000US-0232401 2000US-0233063

14-SEP-2000; 14-SEP-2000;

AAK69779;

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AAK69779 RESULT

08-DEC-2000;

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2000US-0236802.
2000US-0237037.
2000US-0237038.
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2000US-0241785.
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2000US-0246474.
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2000US-0249212.
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2000US-0236370.
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2000US-0246528.
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2000US-0251988
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2000US-0251868
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26 - SEP - 2000;
27 - SEP - 2000;
28 - SEP - 2000;
29 - SEP - 2000;
20 - CCT - 2000;
20 - C
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06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) and addition acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome complement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the rucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK84950 and AAM82169 represent invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 24591; 3071pp + Sequence Listing; English.
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Pred. No. 1.4e-40;
0; Mismatches 15;
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2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0254097.
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94.2%;
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                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 94.2
Matches 242; Conservative
                                                                                                                                                   Barash SC,
                                                                                                                                                                                      WPI; 2001-483426/52.
                   08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
                                                                                                                                                   Rosen CA,
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AAK73320
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2000US-0236367
2000US-0236368
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2000US-0236370
2000US-0237039
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                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                              AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

activity, and can be used in gene therapy and vaccine production. (I)

proteins and polynucleotides may be used in the prevention, diagnosis and

treatment of diseases associated with inappropriate (I) expression. For

example, they may be used to treat disorders associated with decreased

cypression by rectifying mutations or deletions in a patient's genome

that affect the activity of (I) by expressing inactive proteins or to

supplement the patients own production of (I). Additionally, (I)

cypolynucleotides may be used to produce the secreted (I), by inserting

the nucleic acids into a host cell and culturing the cell to express the

protein. (I) proteins and polynucleotides may be used to prevent,

cancers and cancer metastases of haematopoietic active cells. AAK64703

cancers and cancer metastases of haematopoietic antigen genomic

to AAK87694 represent human immune/haematopoietic antigen genomic

sequences from the present invention. AAK54912 to AAK54950 and AAM82169

cypresent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18263 tgcgcttctccttgctgtaatttcagacccggatgcagagtctacagcctgacccagctg 18322
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Pred. No. 1.4e-40;
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33.6%; Score 233; DB
Best Local Similarity 94.2%; Pred. No. 1.4e
Matches 242; Conservative 0; Mismatches
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11-DEC-2000; 2000US-0254097. 05-JAN-2001; 2001US-0259678.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y. Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
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tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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Wejhrman T, Goodrich R;
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62.9%;
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01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0663561.
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27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
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Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAM79039
                                                                                                                                                                        WO200157190-A2
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cgttttccaccaccaaggaaacagccacctagccaacgggatagctgggagtatggccac 416

ВР

(first entry)

tgtaatccaccctgggggggaatagccatattgccaatggtgcggccgggtgtgtgggcaac

542

tataagaacggagggcctatggaggcccatgagggggctgaacgtcacagcaacaggcgc

gagtetacageetgaeceagetgeeegetategeaatgtgttggaggeeetetggaggat

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543 attacttcatgatgcagccatgaaccctgcggaag 577
                                                                                                                                                                      AAH90057 standard; cDNA; 2562
                                                                                                                                                                                                                                                                        Human bone marrow cDNA,
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                                                                                                                                                                                                                                      AAH90057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel human mitochondrial solute carrier protein, hMSC-o (AAB60658), and cDNA encoding it (AAF59920). hMSC-o is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-o proteins and nucleic acids, and the detection of hMSC-o proteins and nucleic acids, and the sequence represents cDNA encoding hMSC-o.
New human mitochondrion solute carrier protein and its nucleic acid
                                        1340 aatcatgcggaccgaaggcttctggaggcccttgcgaggcgtcaacgtcatgagg
                         gattataagaacggagggcctatggaggccatgagggggctgaacgtcacagcaacagg
                                                         cgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattgag
                                                                                          tgatgtaatccaccctggggggaatagccatattgccaatggtgcggccgggtgtgtgggc
                                                                                                                                                                                                                                                      solute carrier protein; hMSC-o; hypothalamus;
                                                                                                                                                                                                                                     Human mitochondrial solute carrier protein hMSC-o cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1305 BP; 292 A; 388 C; 363 G; 262 T; 0 other;
                                                                                                                                   540 aacattacttcatgatgcagccatgaacctgcggaag 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 19-20; 21pp; Chinese.
                                                                                                                                                                                    BP,
                                                                                                                                                                                   AAF59920 standard; cDNA; 1305
                                                                                                                                                                                                                                                                                                                                                              (SREN-) SOUTHERN RES CENT NAT
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                                                                                                                                                                                                                                                                                                                                              17-MAR-2000; 2000CN-0114958
                                                                                                                                                                                                                                                              detection; ss
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                                                                                                                                                                                                                                                      mitochondrial
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                                                                                                                                                                                                                                                               preparation;
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Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful
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disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel bone-marrow-expressed polynucleotides and for treating e.g. cancer and immune deficiency
SEQ ID NO: 301.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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2000US-0250583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
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P-PSDB; AAM00938
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03-AUG-2000;
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Ren F, W
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Length 1305;

DB 22;

28.4%; Score 196.6; DB 22; 68.6%; Pred. No. 5.6e-33; iive 0; Mismatches 124;

Conservative

Local Similarity es 271; Conserv

Best Loca Matches

183 57

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Query Match

242

243 ggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaagacccggatgca 302

ggactacgaggcgctggagccactgtcaccacgcactggtggcaggcgccgt

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polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzhaimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1920 tgccgactagcgcctccgtgtccacccacatgacagcaggagcgatggccgggatcctgg 1979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2562 BP; 623 A; 660 C; 627 G; 652 T; 0 other;
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Pred. No. 5.6e-31;
                                                                                                                                                                                                                                                                                                                                                                                             chemical compounds as potential drugs.
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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Matches 260; Conservative
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I). by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
to AAK89694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK8950
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ή.
                                                                                                                                                                                                                                                                                                                   represent sequences used in the exemplification of the present invention
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                         26.1%; Score 181; DB 22; Length 339; 95.1%; Pred. No. 1e-29; tive 1; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                    Sequence 339 BP; 86 A; 84 C; 101 G; 64 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human full-length cDNA, SEQ ID NO: 4109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 gacattgagtgatgtaatccaccct 495
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Matches 195; Conservative
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P-PSDB; AAM85891.
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Claim 2; SEQ ID NO 817; 1380pp + sequence listing; English.
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                                                                                                                                                                                           Wakamatsu A, Sugiyama T, Nagai
                                                                     07-JUL-2000; 2000EP-0114089.
                                                                                                         11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
                                                                                                                                                    (HELI-) HELIX RES INST
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                                                                                        The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA assily without any special methods. The present sequence is a full length enrich.
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                          Primers useful for synthesizing full length cDNA clones and their
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                                                                                                                                                                                                                                                                                                                                             Gaps
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specification, but was obtained in CD-ROM format directly from EPO
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                                                                                                                                                                                                                                                                                                                 DB 22; Length 1890;
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                                                                  Claim 8; SEQ ID NO 4109; 1380pp + sequence listing; English
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                                                                                                                                                                                                                                                                                                               25.1%; Score 174.2; DB 22; Length 62.4%; Pred. No. 3.6e-28; ive 0; Mismatches 173; Indels
                                                                                                                                                                                                                                                                         Sequence 1890 BP; 441 A; 534 C; 496 G; 419 T; 0 other;
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 ggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgccgt 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaagacccggatgca 302
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Primers useful for synthesizing full length cDNA clones and their

in genetic manipulation -

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Hayashi K, Ishii S, Kawai Y; K, Kojima S, Otsuki T, Koga

Isogai T,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16,
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Sequence 1
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Sequence 1,
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Sequence 4
Sequence 3
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                      Compugen Ltd
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US-09-165-264-14

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US-09-165-264-11

US-08-510-646B-3

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US-08-103-840A-1
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US-08-893-333-1
US-08-054-077C-1
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US-08-483-533-39
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                        September 28, 2002, 07:54:54
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Maximum Match 100%
Listing first 45 summaries
                                                                                                nucleic search, using sw model
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length: 2000000000
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Maximum DB
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Sequence 15, Appli
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Sequence 36,
Sequence 36,
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Sequence 3
Sequence 2
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Pred. No. 5.5e-06;
0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis;
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 8 Patentin Ver. 2.1
SEQ ID NO 8 Patentin Ver. 2.1
LENGTH: 319
US-09-283-471A-39
US-08-658-136-1
US-08-658-136-1
US-08-658-136-1
US-09-283-471A-36
PCT-US91-06532-1
US-08-458-745-1
US-08-458-745-1
US-09-458-568A-11
US-09-458-568A-11
US-09-773-816-1
US-09-773-816-1
US-09-773-816-1
US-09-775-891B-24
US-08-903-800A-3
US-08-603-8838-1
US-08-603-8838-1
US-08-603-8838-1
US-08-60-8838-1
US-08-406-030-3
US-08-60-8838-1
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                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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US-09-165-264-12
Sequence 12, Application US/09165264
Setent No. 619710
GENERAL INFORMATION:
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US-09-128-155-16/c
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                                                                                                                                                                                                                           gagococoggogategococtoctogacogogtogoctocaocogogocotogogococogogoc 122
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US-09-165-264-14
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Pred. No. 5.1e-05;
0; Mismatches 138; Indels
                                                                                                                                   Length 318;
                                                                                                                                Query Match 8.4%; Score 58.2; DB 4; Length 3 Best Local Similarity 61.6%; Pred. No. 5.1e-05; Matches 93; Conservative 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-165-264-14
US-09-165-264-14
Sequence 14, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TILE REFERENCE: 44747
CURRENT APPLICATION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
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                                                                                                                                                                                                                                                                                                                   Query Match 8.4%;
Best Local Similarity 50.5%;
Matches 141; Conservative (
                             TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 14
LENGTH: 320
SEQ ID NO 12
LENGTH: 318
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                                                           FEATURE:
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128 goggggaggccggggcctgcaggccccggtacgacaagatccggactccggcccggact 187
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                                                               TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF ELLE REFERENCE: 09404/05201 CURRENT APPLICATION UNABER: US/09/128,155 CURRENT FILING DATE: 1998-08-03 EARLIER APPLICATION NUMBER: US 60/091,650 EARLIER APPLICATION NUMBER: US 60/054,646 EARLIER FILING DATE: 1998-07-08-04 EARLIER FILING DATE: 1997-08-04
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APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis;
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT APPLICATION NUMBER: US/09/165,264
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%; Score 57.8; DB 4; ilarity 61.7%; Pred. No. 6.3e-05; Conservative 0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58.2; DB 3;
Pred. No. 0.00018;
0; Mismatches 93;
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SEQ ID NO 16
LENGTH: 152331
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Sequence 16, Application US/09128155 Patent No. 6117654
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; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 55.1%;
Matches 114; Conservative
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FEATURE:
NAME/KEY: misc_feature
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Best Local Similarity
Matches 92; Conserv
                                                GENERAL INFORMATION:
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US-09-165-264-7
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61.9%; Pred. No. 7.7e-05;
tive 0; Mismatches 56;
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ORGANISM: S.pristinaespiralis
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IBM PC compatible
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REGIESTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Blanche, Francis
Crouzet, Joel
Jacques, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lacroix, Patricia
                                                                                                                                                                                                                                                                                                                                                                                               Blanc, Veronique
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thibaut, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           833 base pairs
                       91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
     Best Local Similarity
Matches 91; Conserva
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                     US-08-403-852D-3/c
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APPLICANT:
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APPLICANT:
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                                    63 gagccccgggggagtcggcgctgctggacgggtggctgcagcgggggcgtgggccggggggc 122
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Primer sequence US-09-165-264-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%; Score 57.6; DB 4; Length 320;
58.9%; Pred. No. 7e-05;
Live 0; Mismatches 69; Indels
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Patent No. 6197510

GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah

TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747

CURRENT APPLICATION NUMBER: US/09/165,264

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: 320
                                                                                                                                                                                                                                                                                                                               APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REPERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%; Score 57.4;
                                                                                                                                                 123 cggcggcgggaggccggggcctgcaggc 151
                                                                                                                                                                                   276 ggggggggggggggggggggggggggg 304
                                                                                                                                                                                                                                                                            Sequence 13, Application US/09165264
Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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Matches 99; Conservative
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                                                                                                                                                                                                                                            RESULT 6
US-09-165-264-13
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FEATURE

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APPLICANT: Debussche, Laurent
APPLICANT: De Crey-Lagard, Valerie
APPLICANT: De Crey-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
                                                                                                                                                                          63 gagccccgggggagtcggcgctgctggacgggtggctgcagcgggggcgtgggccggggggc 122
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1300 I Street, N.W., Suite 700
Indels
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SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
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US-09-231-818-3/c
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US-08-510-646B-3
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VENTION: Polypeptides Involved In The
BIOSYNCHESIS Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
                                                                                                                                                                                                                  119 gggccggcggcggggggggggcctgcaggcccccggtacgacaagatccggactccg
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                                                                                                                                                                                                                                                                                                                667 CGGCGGCCAGTTCGGCCGGCCGGGCAGCGCCAGGAGGATCTTGGCGTGCGGTGCCT
                                                                                                                      4
                                                                                  Score 50.6; DB 2; Length 833;
Pred. No. 0.0034;
0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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FILING DATE: 25-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
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APPLICATION NUMBER: US 08/403,852
FILIAN DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
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Patent No. 6077699
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Thibaut, Denis
Zagorec, Monique
Debussche, Laurent
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                                                                                   7.3%;
53.0%;
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Crouzet, Joel
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                                                                                Query Match 7.3°
Best Local Similarity 53.0°
Matches 133; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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; NAME/KEY;
; LOCATION:
US-08-403-852D-3
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APPLICANT:
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APPLICANT:
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APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Zagorec, Monique
APPLICANT: Zagorec, Monique
APPLICANT: De Creoy-Lagard, Valerie
APPLICANT: De Creoy-Lagard, Valerie
APPLICANT: De INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 gggccggcggcgggggggggggcctgcaggcccccggtacgacaagatccggactccg 178
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1300 I Street, N.W., Suite 700
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                                                                                               03806.0054-01000
                                     NAME: Meyers, Kenneth J.
REGIZFRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEC ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/09231818; Patent No. 6171846; GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth T
                                                                                                                                                                                                                                                                  LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.33
Best Local Similarity 53.03
Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-CENA
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CITY: Washington
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Nathalie
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Best Local Similarity 53.0%;
Matches 133; Conservative C
  Francis
                                                                              Denis
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LENGTH: 5392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSE: Finnegan,
                                                                                                                                                     TITLE OF INVENTION: PTITLE OF INVENTION: BTITLE OF INVENTION: CANDER OF SEQUENCES:
                                                       Lacroix, Thibaut,
Blanche,
                                       Jacques,
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ZIP: 20005-3315
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ORIGINAL SOURCE
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                                                                          APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/231,818
                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: PR 92/11441
FILING DATE: 25-SEP-1992
ATORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
RELEPRANCE CAGOO TELEFAX: (202) 408-4400
TELEFAX: (202) 408-4400
TELEFAX: (202) 408-4400
TELEFAX: (202) 408-400
                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Sequence 1, Application US/08403852D
Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 133; Conservative
                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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                                                                                           OPERATING SYSTEM:
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ORIGINAL SOURCE
                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                        Biosynthesis Of Streptogramins, Nucleotide S
Coding For These Polypeptides And Their Use
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                                                                                                                                                                                                                                Garrett & Dunner
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                                                                                                           Polypeptides Involved In The
Biosynthesis Of Streptogramin
                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
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Pred. No. 0.0049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                           SEE: Finnegan, Henderson, Farabow, 1300 I Street, N.W., Suite 700 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                          De Crecy-Lagard, Valerie
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                          Zagorec, Monique
Debussche, Laurent
Patricia
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3238 CGAGGCGGGG 3228
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CITY: Washington
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APPLICANT: Lacroix, Patricia
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: Debussche, Laurent
APPLICANT: De Crey-Lagard, Valerie
APPLICANT: De Crey-Lagard, Valerie
TITLE OF INVENTION: Polypeptides involved in The
TITLE OF INVENTION: Biosynthesis of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-804-1995
CLASSIFICATION 3-804-1995
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 2-SEP-1993
PRIOR APPLICATION NUMBER: FR 92/11441
FILING DATE: 2-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 2-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   Sequence 1, Application US/08510646B
Patent No. 6077699
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TELEFAX: (202) 408-44000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    Blanc, Veronique
Blanche, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                  Crouzet, Joel
                                        3238 cGAGGGCGGGG 3228
239 ccgtggcaggg 249
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
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20005-3315
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                                                                                                                              US-08-510-646B-1/c
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US-08-510-646B-1
                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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Gaps

4

7.3%; Score 50.6; DB 3; Length 5392; 53.0%; Pred. No. 0.0049; live 0; Mismatches 114; Indels 4

Conservative

Best Local Similarity Matches 133; Conserv

Query Match

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APPLICANT: Jacques, Nathalie
APPLICANT: Jacques, Nathalie
APPLICANT: Thibaut, Denis
APPLICANT: Applicant: Jacore, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Trecy-Lagard, Valerie,
APPLICANT: De Trecy-Lagard, Valerie,
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
                                                 3298 GCTGCTTCACCGAGGCGGCGTCGGCCGCCTCGTCGAGGAGGACGAGGTCGGCGGCCGCGG 3239
                                                                                                                                                                                                                                                                           3358 CGGCGGCAGTTCGGCGGCCGGGCCGGCAGGCAGGAGGATCTTGGCGTGCGGTGCCT 3299
                                                                                                                                                                                                                 119 gggccggcggcggggggccgggggcctgcaggcccccggtacgacaagatccggactccg 178
                                                                                                           179 gcccggactacgagggcgctgcggctggagccactgtcaccacgcacatggtggcaggcg 238
E: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
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APPLICATION NUMBER: US/08/403,852
FILING DATE: 10.MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5392 base pairs
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LENGTH: 5392 base pair:
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STRANDEDNESS: single
                     linear
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                                  MOLECULE TYPE:
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                                                                     NAME/KEY:
                                                                                         LOCATION:
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                                                                                                                                           LOCATION:
                                                                                                                                                           FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-804-227C-1
                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                  119 gggccggcggggggggggggggctgcaggccccgggtacgacaagatccggactccg
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                                                                                                                                                                                         Query Match 7.3%; Score 50.6; DB 4; Length 5392; Best Local Similarity 53.0%; Pred. No. 0.0049; Matches 133; Conservative 0; Mismatches 114; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08804227C; Patent No. 5876991
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Minberly S.
APPLICANT: Rotteck, Paul R., Jr.
APPLICANT: Sotten, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
ODPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: 35,784
REFERENCE/DOCKET NUMBER: 3-8231
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                       ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 43280 base pairs
TYPE: nucleic acid
              double
          STRANDEDNESS: GOUD:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3238 CGAGGCGGGG 3228
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                                                              <u>Q</u>
                                                                                ANTI-SENSE: NO ORIGINAL SOURCE:
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16378 CCTGCCCGACGGGCCCGTCTGGTGGCCGCGGGGGCGCTGATGCAGGCCCTGCCGGC 16437
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APPLICANT: RHEE, Sang-Ki
APPLICANT: CHOI, Eui-Sung
APPLICANT: CHOI, Eui-Sung
APPLICANT: KIM, Chul-Ho
APPLICANT: KIM, Houn-Ho
APPLICANT: KIM, Hav-Young
TITLE OF INVENTION: AUTONOMOUSLY REPLICATING SEQUENCES,
TITLE OF INVENTION: GAPDH GENE AND PROMOTER DERIVED FROM
TITLE OF INVENTION: HANSENULA POLYMORPHA, EXPRESSION
TITLE OF INVENTION: THE SELECTION OF TRANSFORMANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: RHEE, Sang-Ki
STRREET: KeukGong Villa Ka-101, Kwangjang-dong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                             Length 43280;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 49.4; DB 2; Length 4
Pred. No. 0.014;
0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08903800A Patent No. 5935789
                                                                                                                                                                                                                                                                                                                                                                                                               7.18;
50.28;
DNA (genomic)
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816..14234
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Pred. No. 0.024;
0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 302-280
ADDRESSEE: KANG, Hyun-Ah
STREET: Kyungseong Keunmaul Apt. 125-1501, Kalma-dong,
STREET: Seo-gu
                                                                                                                                                    ZIP: 305-335
ADDRESSEE: KIM, Chul-Ho
STREET: Shindonga Apt. 2-1101, Yongjeon-dong, Dong-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Secon1
CONTRE! Secon1
CONTRE! Republic of Korea
ZIP: 120-190
COMPUTER READABLE FORM:
MEDTUM TYPE: Diskette, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/AT
OPERATIOS SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,800A
FILING DATE: 31-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 97-3173
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Daejon
STATE: Daejon
COUNTR: Republic of Korea
ZIP: 302-171
ADDRESSEE: KIM, Hwa-Young
STREET: #3462, Bukahyun-3-dong, Seodaemun-gu
CITY: Seoul
                                                                                                                                                                                                                                                                         ZIP: 300-200
ADDRESSEE: SOHN, Jung-Hoon
STREET: Nuri Apt. 103-506, Wolpyung-dong, Seo-gu
                                  ADDRESSEE: CHOI, Eui-Sung
STREET: Dasol Apt. 102-507, #395-3, Kung-dong,
STREET: Yuseong-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
Republic of Korea
                                                                                                                      RY: Republic of Korea 305-335
                                                                                                                                                                                                                          COUNTRY: Republic of Korea AIP: 300-200
                                                                                                                                                                                                                                                                                                                                              STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 302-280
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SEQUENCE CHARACTERISTICS:
LENGTH: 1227 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: genomic DNA
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Best Local Similarity 59.4%;
Matches 98; Conservative.
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Job time: 11228 sec
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62 ggagccccgggggagtcggcg--ctgctggacgggtggctgcagcgggggcgtgggccggggg 119

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BI827322 603077989

Perfect score:

Run on:

Sequence:

Scoring table:

Minimum DB Maximum DB

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vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland. 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com"
824 c 322 g 139 t 15 others
                                                                         AA104365 mp01966.r
B1412175 602965377
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AL530804 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD008YH17 5
AL530804
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Uni,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 888
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Homo sapiens
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JOURNAL
COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
AL530804
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; Search time 4881.77 Seconds
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           4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                  13736207 seqs, 6748477542 residues
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Copyright (c) 1993 - 2000
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Maximum Match 100%
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/organism="Mus musculus"
Plate: LLAMILLZV .....
High quality sequence stop: 7
Location/Qualifiers
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Mus musculus
                                                                                                                                                                                           Similarity
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lonpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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602888838F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5043992
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                              Length 888;
                                                  Indels
                              6
                            Score 532.6; DB 9
Pred. No. 1.1e-93;
3; Mismatches 4.
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                             76.9%;
98.1%;
                                                 Conservative
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BI103329
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                                       Best Local Similarity
Matches 567; Conser
                              Query Match
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RESULT

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1131 bp mRNA linear EST 21-FEB-2001 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4504638 5',
                                                                                                   Site_1: NotI;
imer: Oligo dT
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Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acgggtggctgcagcgggggcgtgggccggggggccggcggcgggggaggccggggcctgca 148
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Pred. No. 1e-77;
0; Mismatches 48;
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BI541703.1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="retina"
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/lab="retina"
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                                                                                                                                                  Contect: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM10377 row: c column: 07
High quality sequence stop: 753.
Location/Qualifiers
rce
                                                                           NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CCACGCACATGGTGGCGGGGGCGCGGGGATCCTGGAGCATTGCGTGATGTACCCGA
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Bovidae; Bovinae; Bos.

1 (bases 1 to 573)

Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the .minscore 18 and .minmatch 12 options.
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            EST 30-AUG-2001
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
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573 bp mRNA linear 455541 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
BI541703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 419.4; DB 1 Pred. No. 9.4e-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 121 row: O column: 24
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 697)
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs.remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
to an incomparation of the plate: LLAMINg Tow: i column: 17
High quality sequence stop: 696.
Location/Qualifiers
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/clone=lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 409.8; DB 10; Length
Pred. No. 6.9e-70;
0; Mismatches 57; Indels
                                                                                                                                                                   tacttcatgatgcagccatgaaccctgcggaag 577
                                                                                                                                                                                   /organism="Mus musculus"
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88.9%;
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EST 20-SEP-2001
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 967)
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
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                                            242 GGGGCCGGCGGCGGGGGGCGTATCAGCCCCTGTACGGCTGGATCCGGAGTCC
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/db_xref="taxon:10090"
/clone="IMAGE:5369084"
/clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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AUTHORS
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602828996F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983815 5', mRNA sequence.

BG964218

GG14318.1 GI:14351855
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IIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10988 row: p column: 24
High quality sequence start: 2
                                                                                                                                                                                                9999ccggcggcggggggcctgcaggcccggtac-gacaagatccggactc
                                                                                                                                                                                                            cggagccccgggggagtcggcgctgctggacgggtggctgc---agcggggcgtgggccgg
                                                                                                                                                                                                                                                                                          cgccgtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaagacccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: gapbs remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                               9
                                                        Length 967;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
this is a NIH_MGC Library."
'8 c 348 g 187 t
                                                                               48;
                                                     Score 398.2; DB 3
Pred. No. 1.3e-67;
0; Mismatches 48
                                                        57.5%;
89.8%;
         278 c
                                                                           Matches 473; Conservative
 Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
           Ø
         154
                                                        Query Match
Best Local 3
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ORGANISM
         BASE COUNT
ORIGIN
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TITLE
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COMMENT
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KEYWORDS
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                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:498815"
/clone=lib="NCI_CGAP_CO24"
/lab_host="blub(B [T] phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="organization"
/note="organizat
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Sus scrofa

Sus scrofa

Sus scrofa

Sus scrofa

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 397)

Fahrenkrugh,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.

Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 cgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgccgtggcagg 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gatcctggagcactgcgtgatgtaccccatcgactgcgtcaagacccggatgcagagtct 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Design and use of two pooled tissue normalized cDNA libraries EST discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 acagectgaececagetgecegetategeaatgtgttggaggeeetetggaggattataag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
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121949 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence
BE012482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 386.6; DB 10; Length
Pred. No. 2.2e-65;
0; Mismatches 39; Indels
                                                                                                                               /organism="Mus musculus"
/strain="FVB/N"
stop: 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 tcatgatgcagccatgaacctgcggaag 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE012485.1 GI:8273406
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Best Local Similarity 91.3%;
Matches 410; Conservative
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Source
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COMMENT
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  AUTHORS
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             TITLE
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                                                         Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 574)
                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 ctgcgtcaagacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgt 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                          9c999gcgtgggccgggggccggcggcggcgggaggccggggcctgcaggccccggtacg 161
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               2 GCGGGGCGTGGGCCGGGGGCCAGCGGGGGGGGGGGGCCTGCAGGCCCCCGGTAAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI185580 574 bp mRNA linear EST 1 UNL-P-FN-Cy-f-02-0-UNL.S1 UNL-P-FN Sus scrofa cDNA clone UNL-P-FN-Cy-f-02-0-UNL 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                           Length 397;
                                                                                                                                                                                                                                                                                                                                                   Indels
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                                                                                                          Score 367.2; DB 9
Pred. No. 1.2e-61;
0; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              μ
                                                                                                                                                                                                                                                                            61
                                              Email: smith@email.marc.usda.gov
                                                                                                                                                                                        /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                /organism="Sus scrofa"
                                                                                                                   BACKWARD: GTTTTCCCAGTCACGACG
Plate: 45 row: O column: 20
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                           141 g
                                                                                                                                                                                                                                                                and 30 embryos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI185580 GI:14659989
                                                                                                                                                                                                                                                                                                                          53.0%;
95.5%;
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Best Local Similarity 95.5
Matches 378; Conservative
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/clone="UNL-P-FN-C2-0-UNL"
/clone="UNL-P-FN-C2-0-UNL"
/clone_Ilb="UNL-P-FN-C2-0-UNL"
/dev_stage="ADULT"
/dev_stage="ADULT"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/lab
                                                                                                                                                                                                                                                                                                                                                                                                                                        Emmal: dpomp@unl.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggtggcaggcgccgtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgt 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 GGCCTCTGGAGGATTATAAAAAACGGAGGCCTGTGGAGGCCCATGCGGGGGCTGAACGT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggccctctggaggattataagaacggaggcctatggaggcccatgaggggctgaacgt 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a normalized cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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; Mismatches 20;
Caetano, A.R., Johnson, R.K. and Pomp, D. Generation and sequence characterization (library from swine ovarian follicles Unpublished (2001)
Contact: Pomp, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 t
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                                                                                                                                                                                                                    Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 6883-0908, USA
Tel: 402 472 6416
Fax: 402 472 65362
Email: dpomp@unl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_SEQ=None found"
171 c 165 g
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Best Local Similarity 94.6%;
Matches 388; Conservative C
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141
                                  EST
                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                 source
LOCUS
DEFINITION
                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                               195
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                    ACCESSION
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                                                         681~\mathrm{bp} mRNA linear EST 09-OCT-2000 ADB Homo sapiens cDNA clone ADBAFE05 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                         gggggccggcggggggggggggggcctgcaggccccggtacgacaagatccggact 175
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                              others
                                                                                                                                                                      Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                              /tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SoLR"
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                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADBAFE05"
/clone_lib="ADB"
                                                                                                                                                                                                                                                                 205 g
                                     AV704087.1 GI:10721407
                                                                                                                                                                                                                                                                 209 c
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                                                     human.
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                                             EST
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                  LOCUS
DEFINITION
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Matches
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/clone_lib="NCI_CGAP_Mam1"
/clone_lib="NCI_CGAP_Mam1"
/dev_stage="type="tuncr, biopsy sample"
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/lab_host="Nome months, virgin"
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/note="Organ: mammary; Vector: pcWV-SPORT6; Site_1: SalI;
/inche="Organ: mammary; Vector: pcMV-SPORT6; Site_1: SalI;
/inche="Organ: pcMV-SPORT6; Site_1: SalI; SalI;
/inche="Organ: pcMV-SPORT6; Site_1: SalI; S
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 598)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9146 row: o column: 17
High quality sequence stop: 593.
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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Matches 359; Conserv
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RESULT 1 BE913718

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Gaps

0;

Indels

SOURCE ORGANISM

KEYWORDS

VERSION

REFERENCE AUTHORS

ACCESSION

TITLE JOURNAL COMMENT

LOCUS DEFINITION RESULT 12

BI794616

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BI045863 480 bp mRNA linear EST 14-JUN-2001
MR3-FN0209-300101-004-h10 FN0209 Homo sapiens CDNA, mRNA sequence.
BI045863
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-FN0209-30010-004-hl0&t3=2001-01-30&t4=1)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with \ensuremath{\mathsf{ORF}} expressed sequence tags
                                                                                                                                                                                                                            335 gcaatgtgttggaggccctctggaggattataagaacggaggcctatggaggcccatga 394
                                                                                                                                                                                                                                                                                                                                                                                                                            395 ggggggtgaacgtcacagcaacaggcgcagggcctgcccacgccctttattttgcctgct 454
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                                                                                                                                                                                               275 ccatcgactgcgtcaagacccggatgcagagtctacagcctgacccagctgcccgctatc 334
                                                                                                                                           1 TCACCACGCACATGGTGGCGGCGCCGTGGCAGGGATCCTGGAGCATTGCGTGATGTACC 60
                                                                                       tcaccacycacatggtggcaggcgccgtggcagggatcctggagcactgcgtgatgtacc
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20202663
  4.7e-53;
                             Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0209"
        Pred. No.
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High quality sequence stop: 480
Location/Qualifiers
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  93.1%;
Best Local Similarity 93.1
Matches 338; Conservative
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                            SM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 560)
S Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,
M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTS: 1692e0.x1
                                                                                                                                     BI794616 560 bp mRNA linear EST 01-OCT-2001 ic92e02.yl Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus cDNA 5' similar to TR:Q23125 Q23125 W02B12.9 PROTEIN. [1]; mRNA sequence.
BI794616
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: dmeltonebiohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Mashington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brownefas.harvard.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 430.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Melton Normalized Mixed Mouse Pancreas 1 NI-MMS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/db_xref="taxon:10090"
  361 TGCAGCCATGAATCCAGCGGAAG 383
                                                                                                                                                                                                                                                                             BI794616.1 GI:15822341
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source

FEATURES

Query Match

BASE COUNT ORIGIN

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                                                           FEATURES
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1 (bases i to 336)

Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
               puc18; Site_1: SmaI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 25-APR-2001
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
                                                                                                                                                                                                                                 346 gaggecetetggaggattataagaacggagggeetatggaggeecatgagggggetgaac 405
                                                                                                                                                                                                                                                                                                          406 gtcacagcaacaggcgcagggcctgcccacgccctttattttgcctgctacgaaagtta 465
                                                                                                                                                                                                                                                                                                                                                                                                                               286 gtcaagacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttg 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 aaaaagacattgagtgatgtaatccaccct-gggggcaatagccatattgccaatggtgc 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 AAAAAGACATTGACTGATGAATCCACCCTGGGGGGCAATAGCCATATTGCCAATGGTGC 301
                                                                                                                                                                                                          1; Gaps
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Pred. No. 1.6e-52;
0; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW326482 336 bp mRNA linear 19106 MARC 1BOV Bos taurus CDNA 5', mRNA sequence. AW326482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TED: 402 762 4366
Fax: 402 762 4390
                                                                                                                 146 g
/dev_stage="Adult"
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                                                                                                                                                                          46.2%;
96.0%;
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VERSION
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BM488747

pgm2n.pk008.12 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate CDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk008.12 5' similar to ref[XP_050766.1 (XM_050766)] putative mitochondrial solute carrier [Homo sapiens] putative mitochondrial solute carrier [Homo sapiens] carrier splice variant [Homo sapiens] w mNNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                              /note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary." 96 c 107 g 61 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgaaaagttaaaaaagacattgagtgatgtaatccaccctgggggcaatagccatattgc 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 caccacgcacatggtggcaggcgccgtggcagggatcctggagcactgcgtgatgtaccc 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catcgactgcgtcaagacccggatgcagagtctacagcctgacccagctgcccgctatcg 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caatgtgttggaggccctctggaggattataagaacggagggcctatggaggcccatgag 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggggctgaacgtcacagcaacaggcgcagggcctgcccacgccctttattttgcctgcta 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 TGAAAAGTTAAAAAAGACATTGAGTGATGTAATCCACCCTGGGGGCAATAGCCATATTGC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 CACCACGCACATGGTGGCGCGCGCGCGGGGGTCCTGGAGCACTGCGTGATCTACC 73
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 302.2; DB Pred. No. 5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cogburn, L.A. and Monsonego-Ornan, E.
                                                                                                                                                                                                /clone_lib="MARC_1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                     /organism="Bos taurus"
/db_xref="taxon:9913"
                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 8 row: F column: 16
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                  Location/Qualifiers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM488747.1 GI:18609678
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96.0%;
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us-09-870-113-5.rst

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Jacustages Breast, leg:Embryo(d19); post-hatch(ld,1,3,5,7,9,11 weeks); growth plate(ld,7d,14d post-hatch) | Jalbahost="E. coli EMDH10B; fill and the post-bactor of total RNA isolated from each tissue (embryonic macle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                            /db_xref="taxon:9031"
/clone="pgm2n.pk008.12"
/clone="pgm2n.pk008.12"
/clone=lb="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate CDNA library (pgm2n)"
/sex="Male and Female"
                                                                                                                                                                                                                     /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCCGGAGCCGCGCTCGCCG---CCCGCCCCGACTACGAGGCCGCTGCCGCAGGGCGCC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 actgicaccacgcacatggiggcaggcgcgiggcagggatcciggagcactgcgtgatg 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 cccccggtacgacaagatccggactccggcccggactacgaggcgctgccggctggagcc 210
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                                                                                                    Ottawa Res. Centre
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                                                                                                                                                                                                                                                                                                                                                                                      6 others
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Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
                                                                                                    and
                                                                  1. .546
/organism="Gallus gallus"
/strain="Commercial broiler
Strains 90 & 21"
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Search completed: September 28, 2002, 06:22:41 Job time: 9182 sec

Scoring table:

Searched:

Minimum DB s Maximum DB s

Database

Perfect score:

Sequence:

OM nucleic

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AX012190 Sequence 028167 human STS S AX003265 Sequence 26651 Caenorhabdi AV060268 Drosophil 045998 Onchocerca AX198694 Sequence AX209226 Sequence AF217402 Drosophil AF21674 Homo sapi
                                                Aj303077 Homo sapi
AF327403 Homo sapi
Aj303078 Homo sapi
AF267854 Homo sapi
AL353719 Human DNA
AK056782 Homo sapi
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AF223466 Homo sapi
AF361699 Mus muscu
AF15560 Homo sapi
AY032628 Homo sapi
AC00878 Mus muscu
AC051642 Homo sapi
AC022597 Homo sapi
AF216674 Homo sapi
AX012190 Sequence
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BC015013 Homo sapi
G22871 human STS W
X56445 Yeast nucle
X49408 S.cerevisia
X87771 S.cerevisia
AX316750 Sequence
AX011696 Sequence
Z28277 S.cerevisia
X5644 Yeast nucle
AC019588 Drosophill
AC009388 Drosophill
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BC023172 Mus muscu
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AX306258 Sequence
AX071440 Sequence
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Lal, P., Yang, J., Yue, H., Hillman, J.L., Tang, Y.T., Bandman, O., Burford, N., Baughn, M.R., Azimzai, Y., Lu, D.A., Au-Young, J. and Patterson, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE003763 Drosophil
          Seguence
     AX061229 :
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Patent: WO 0078953-A 76 28-DEC-2000;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Sequence 76 from Patent WO0078953.
AX061229 GI:12406365
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                              AF327402
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AF327403
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AF2346621
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AX011696
SCYKR052C
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AY060268
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ORGANISM
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VERSION
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JOURNAL
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AUTHORS
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AX061229
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                                                                                                                                                                    ; Search time 5287.54 Seconds (without alignments) 3158.251 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                  1 atgcagagtctacagcctga.....agtggagggctggcaagtga
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                    September 28, 2002, 07:55:42
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Listing first 45 summaries
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DVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRRAWGN
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AATTPLDVCKTLLNTQESLALNSHITGHITGHASAFRFVYQVGGVTAYFRGVQARVIY
OPESTALAMSVYEFKYLTKRGGEBRAGK"
408 c 235 g 283 t
                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1448)
Li,F., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R.
Lissson,C. and Suomalainen,A.
Direct Submission
Submitted (08-DEC-2000) Human Molecular Genetics, National Public Health Institute, Mennerhelmintie 166, Helsinki 00300, Finland
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1448)

Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R., Larsson,C. and Suomalainen,A.

Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing
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llarity 100.0%; Pred. No. 7.2e-240;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
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30. 1124
                                                                                                                                       FEBS Lett. 494 (1-2), 79-84 (2001) 21195335
                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAK49519.1"
                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                              proteins 3 and 4
              Homo sapiens
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les 798; Conserv
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                                                        REFERENCE
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Homo sapiens putative mitochondrial solute carrier splice variant mRNA, complete cds, alternatively spliced, nuclear gene for mitochondrial product.

AF327402.1 GI:13926046
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ACCESSION VERSION KEYWORDS .rge

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Larsson C., Suomalainen A.;
"Characterization of a novel human putative mitochondrial transporter
homologous to the yeast mitochondrial RNA splicing proteins 3 and 4";
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Submitted (12-DEC-2000) to the EMBL/GenBank/DDBJ databases.
Nikali K., Human Molecular Genetics, National Public Health
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HMRS3/4 gene; mitochondrial RNA splicing protein 3/4
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(Rel. 67, Last updated, Version 2)
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/db_xref="taxon:9606"
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FEBS Lett. 494:79-84(2001).
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26-APR-2001
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Nikali K.;
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/function="putative mitochondrial solute carrier"
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LDVCKTLLNTQESLALNSHITGHITGMASAFRTVXQVGGVTAYFRGVQARVIYQIPSTA
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                                                                                                                                                                  BP; 322 A; 408 C; 435 G; 283 T; 0 other;
                                                                                                                                                                                                              100.0%; Score 798; DB 17; 100.0%; Pred. No. 7.2e-240;
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                                                                                                                                                                                                                                          0; Mismatches
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Matches 798; Conservative
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li F., Nikali K., Gregan J., Leibiger I., Leibiger B., Schweyen R., Larsson C., Suomalainen A.; "Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing proteins 3 and 4"; FEBS Lett. 494:79-84(2001).
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                                                               463 aacccccagagacggtacaacccaagctcccacgtcctctctggagcttgcgcaggagct
                taccagatccctccacagccatcgcatggtctgtgtatgagttcttcaaatacctaatc
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    /db_xref="taxon:9606"

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NTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYE
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alternatively spliced"
/codon_start=1
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Submitted (08-DEC-2000) Human Molecular Genetics, National Public Health Institute, Mennerhelmintle 166, Helsinki 00300, Finland
Location/Qualifiers
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I (bases I to 1889)
Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R., Larsson,C. and Suomalainen,A.
Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing proteins 3 and proteins 404 (1-2), 79-84 (2001)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q24"
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Matches 576; Conservative
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JOURNAL MEDLINE

PUBMED REFERENCE

REFERENCE AUTHORS

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RESULT AF327403

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/product="NPD016"
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/product="nPD016"
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FKYLITKRQEFWRAGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL353719 123160 bp DNA linear PRI 25-SEP-2001
Human DNA sequence from clone RP11-85A1 on chromosome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 26, 2001 this sequence version replaced gi:14280413.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                    agtggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgt 338
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Catarrhini; Hominidae; Homo
                                                                                                                                                                                    0;
                                                                                                                                                          Length 1244;
                                                                                                                                                                                    0; Indels
                                                                                                                                                        65.2%; Score 520; DB 9; Lv
100.0%; Pred. No. 2.7e-152;
ive 0; Mismatches 0;
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Eukaryota; Metazoa; Chordata; Cj
Mammalia; Eutheria; Primates; Cs
I (bases 1 to 123160)
Ramsay, H.
Direct Submission
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AL353719 AC007643
AL353719.10 GI:15787725
     /codon_start=1
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Best Local Similarity 100.
Matches 520; Conservative
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                                                                                                                                                                                                                                                                       ggtgcggccgggtgtgtgtgcaacattacttcatgatgcagccatgaacctgcggaagtg
                                                                                                                                                                     gtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgtacgg
                                                                                                                                                                                                                        gcagtgtggcaaaatgaaggggccggggccttttaccgcagctacaccagccgacc
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                                                                  Length 1889;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1244)
Xu,X., Yang,Y., Gao,G., Xiao,H., Chen,Z. and Han,Z.
Direct Submission
                                                                                       Indels
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                            other;
                                                                DB 17; L
6.3e-170;
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                                                              cch 72.2%; Score 576; DB sl Similarity 100.0%; Pred. No. 6.3 576; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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                         BP; 404 A; 508 C;
  YLITKRQEEWRAGK"
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                                                                Query Match
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KEYWORDS
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AUTHORS
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, GANISSPROT: Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
RP11-85A1 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                          together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence is not the entire insert of clone RP11-85A1 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP11-85A1 is at 1 in this sequence. The true left end of clone RP11-85A1 is at 1230G1 in this sequence. The true right end of clone RP11-129J12 is at 51589 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82871
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/clone="RPCI-11.1"
complement(7066. 7118)
/note="Single clone region. Sequence from reads from a Short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Where differences are found these are annotated as variations
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/db_xref="taxon:9606"
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Isogal, T., Otsuki, T. and Suglyama, T.

Direct Submission

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
NEDO human cDNA sequencing project supported by Mnistry of
Research Association for Biotechnology (RAB): cDNA full insert sequencing:
Research Association for Biotechnology (RAB): cDNA library
Construction: Helix Research Institute (HRI) (supported by Japan
Rey Technology Center etc.); 5- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
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Ishibashi, T. Kanehori, K., Yosida, M., Watanabe, S., Ishida, S.,
Ishibashi, T., Kanehori, K., Yosida, M., Takiguchi, S.,
Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M.,
Yamashita, H., Chiba, Y., Sugiyama, T. Irie, R., Otsuki, T., Sato, H.,
Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y.,
Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y.,
Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Rawakami, B., Suzuki, Y., Sugano, S.,
NBDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
moderately
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/tissue_type="placenta"
/clone_lib="PLACE6"
/note="cloning vector: pME18SFL3"
1 405 c 375 g 423 t
                                                                                                                                                                                                                                                                     759 aatcactaaaaggcaagaagagtggagggctggcaagtga 798
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99.8%; Pred. No. 8.7e-152;
tive 0; Mismatches 1;
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/db_xref="taxon:9606"
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2 (bases 1 to 1588)
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Matches 519; Conservative
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/clone="MGC:37028 IMACE:4949779"
/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                          /translation="MNPAEVVKQRMQMYNSPYHRVTDCVRAVMQNEGAGAFYRSYTTQ
LTMNVPFQAIHFWTYEFLQEHFNPQRRYNPSSHVLCGACAGAVADAATTPLDVCKTLL
                                                                                                                                                                                                                                                                                                                                           NTQESLALNSNITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYE
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   This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis.
                                                                                                                                                                                                                                               mitochondrial solute
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Pred. No. 2.9e-147;
0; Mismatches 45;
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                                                                                                                                                                                          /note="Vector: pCMV-SPORT6"
188. .721
                                                                                                                                                                                                                                                                          /protein_id="AAH23172.1"
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                                                                                /organism="Mus musculu
/db_xref="taxon:10090'
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1072)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04 FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hulyk, S.W., Hale, S.M.,
Martin, R.G., Muzny, D.M.
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                                                  acgggcagtgtggcaaaatgaaggggccggggccttttaccgcagctacaccaccagct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Lawrence,
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Yoon, V.S., Kowis, C.R., Lawren
Richards, S., Gibbs, R.A.
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MGC.
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Nations.

18. (Dases 1 to 221062)

19. (Dases 1 to 221062)

18. (Dases 2 to 221062)

18. (Daylox S. E. , Amaratunge, H. C., Are, J. R., Banks, T., Barbaria, J., Benton, J., Blimage, K., Blanke, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N.C., Carron, T. F., Carter, M., Cavaco, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Carter, M., Cavaco, S. R., Chacko, J., Chavez, D., Chen, G., Chen, S., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M. D., Daderich, D. A., Delandy, R. T., Daylod, O., Cox, C., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Darper, H., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Darper, H., Coyle, M. D., Dann, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Darper, H., Elantz, P., Garatt, P., Earnhatt, C., Edgar, D., Edwards, C. C., Elbaj, C., Escotto, M., Falls, T., Ferraquto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garbis, H., Garoll, H., Garell, M., Garoll, H., Garell, H., Harlis, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hallis, E., Hamilton, K., Harris, K., Hart, M., Havlak, P., Hawes, A., Jackson, L. E., Jackson, E., Kallson, B., Jak, Y., Johnson, R., Martin, C., Liu, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Martin, R., Martin, R.,
                                AC096351 221062 bp DNA linear HTG 20-DEC-2001 Rattus norvegicus chromosome Rfl clone CH230-24M6, WORKING DRAFT SEQUENCE, 33 unordered pieces.
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On Dec 20, 2001 this sequence version replaced gi:15627972.
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
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Contact: hgsc.help@bcm.tmc.edu
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doss/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pleces arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 205303 bases at least Q30 Consensus quality: 209366 bases at least Q20 Estimated insert size: 209880; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 3.9x in Q20 bases; sum-of-contigs estimation
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 401)
Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.,
Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crain,B.
Human genes and gene expression products
Patent: WO 0102568-A 1912 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                            agtgtggcaaaatgaaggggccggggccttttaccgcagctacaccacccagctgaccat 404
                                                                                                                                                                                                                                                                                                                                                                                                                                          gaacgttcctttccaagccattcacttcatgacctatgaattcctgcaggagcactttaa 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 GAATGTCCCCTTCCAAGCCATTCACTTCATGACCTATGAGTTCCTGCAAGAGCACTTTAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agctgcogcagcoacaaccccactggacgtttgcaaaacactgctcaacacccaggagtc 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 gttaaaaaagacattgagtgatgtaatccaccctgggggcaatagccatattgccaatgg 224
                                                                                                                                                                                                                                                                                              225 tgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaagtggt 284
                                                                                                                                                                                                                                                             15 GTTAAAAAAGACATTGAGTGACGTAATCCACCCAGGGGGCCAATAGCCATATTGCCAATGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    585 cttggctttgaactcacacattacaggacatatcacaggcatggctagt 633
      Patent: WO 0188188-A 1009 22-NOV-2001;
School Juridical Person Nihon University (JP)
Location/Qualifiers
                                                                                                                                                                 Score 417.8; DB 6;
Pred. No. 3.9e-120;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1912 from Patent WO0102568. AX071440
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .401
                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="n = A,T,C or G"
104 c 120 g
                                                                                   /db_xref="taxon:10090"
139 c 121 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                 52.4%;
                                                                                                                                                                                               Matches 437; Conservative
                                                     .483
                                                                                                                                                                                    Best Local Similarity
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AX071440
LOCUS
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ORGANISM
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VERSION
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AUTHORS
      JOURNAL
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525
                                      FEATURES
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                   99151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99390 AGTGGTCAAGCAGCGGATGCAGATGTACACTCACCGTACCACGGGTGACAGACTGTGT 99331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agtggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgt 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aatttaccagatcccctccacagccatcgcatggtctgtgtatgagttcttcaaatacct 758
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99210 CTTTAATCCCCAGAGACGGTACAACCCCAGGCTCCCATGTGCTCTGTGGAGCCTGCGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caggacggtatatcaagtaggtgggtgaccgcctatttccgaggggtgcaggccagagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 ctttaacccccagagacggtacaacccaagctcccacgtcctctctggagcttgcgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agetgtagetgccgcagccaccactggacgtttgcaaaacactgctcaacaccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
Method for examining ischemic conditions
                                                                                                                                                                                                                                                                                           Length 221062;
                                                                                                                                                                                                                                                                                                                            0
215584: gap of unknown length
216996: contig of 1385 bp in length
217059: gap of unknown length
218358: contig of 1289 bp in length
218458: gap of unknown length
219886: contig of 1428 bp in length
21986: gap of unknown length
221062: contig of 1076 bp in length.
                                                                                                                                                                                                                               3487 others
                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 1.6e-135;
0; Mismatches 33;
                                                                                                                                                                /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                             /clone="CH230-24M6"
50577 c 49732 g 58877 t
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WO0188188.
                                                                                                                                                                             /db_xref="taxon:10116"
/chromosome="Rf1"
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1009 from Patent
AX306258
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                                                                                                                                                                                                                                                                                         58.5%;
93.7%;
                                                                                                                                                 .221062
                                                                                                                                                                                                                                                                                                          Best_Local Similarity 93.7
Matches 487; Conservative
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215585
216970
217070
218359
218459
219887
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PAT 25-JAN-2001

linear

RESULT 11 AX306258

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DEFINITION

LOCUS

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE

REFERENCE

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YEFLQEQVNPRRDYNPQSHIISGGLAGALAAAATTPLDVCKTLLNTQENMALSLANVS
GRLSGMANAFRTVYQLNGLAGYFKGIQARVIYQMPSTAISWSVYEFFKYILTKRQLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agtgatgtaatccaccctggggggaatagccatattgccaatggtgcggccgggtgtgtg 240
                                                                                                                                                                                     aggattataagaacggagggcctatggaggcccatgaggggggttgaacgtcacagcaaca 120
                                                                                                                                                                                                   598 tcacacattacaggacatatcacaggcatggctagtgccttcaggacggtatatcaagta 657
                                                                                                                                                           ATGCAGAGTTTGAATCCAGATCCCAAAGCCCGGTATACAAGCATCTATGGCGCCCTCAAG 391
                                                                                                                                                                                                                                    atgcagagtctacagcctgacccagctgccgctatcgcaatgtgttggaggccctctgg
                                                                                                                                                                                                                                                                                                 ATGTACAACTCCCAGCACCAGTCAGCCTTCAGTTGTATCCGGACAGTGTGGGGGACCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aacccaagctcccacgtcctctggagcttgcgcaggagctgtagctgccgcagcaca
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complete cds.
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                                                                                  Score 387.8; DB 10;
Pred. No. 1.3e-110;
0; Mismatches 237;
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Homo sapiens HT015 protein (HT015) mRNA,
AF223466
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                                                                                  Query Match
Best Local Similarity 69.3%;
Matches 543; Conservative C
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                                   BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /produc_t-"mitochondrial solute carrier-like protein"
/pprotein_ld="AAL23899.1"
/db_xref="G1:1650178"
/translation="MELRRGGVGNOAAGRRMDGDCRDGGCGSKDAGSEDYENLPTSAS
YSTHWTAGAMAGILEHSIMYPVDSVYKTRMGSLNDPRRAYFYSTYGALKTMITEGFWR
PLRGLNVAMMAGAGPHAMYRACYENNYETHNDVFSHQGNSHLANGYAGSMATLLHDAY
MNPAEVVKQRLQMYNSQHQSAFSCIRTVWRTGGLGAFYRSYTTQLTMNIPFQSIHFII
                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF288621 4112 bp mRNA linear ROD 27-0CT-2001
Mus musculus mitochondrial solute carrier-like protein mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang, C. - Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SW
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waddy,C.r.
Direct Submission
Submitted (20-JUL-2000) Pathology, University of Florida, 1600
Archer Road, Rm. D6-15, Gainesville, FL 32610, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 247
                                                                                                                                                                                                                                                                                  tacttcatgatgcagccatgaaccctgcggaagtggtcaagcagaggatgcagatgtaca 307
                                                                                                                                                                                   Gaps
                                                                                                                                    taagaacggagggcctatggaggcccatgagggggctgaacgtcacagcaacaggcgcag 127
                                                                                                67
                                                                                8 gtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctggaggatta
                                                                                                                                                                                                                                                                                                         TACTTCATGATGCAGCCATGAACCCTGCGGAAGTGGTCAAGCAGGATGCAGATGTACA
                                                                                                                                                                                                                                   taatccaccetgggggggaatagccatattgccaatggtgcggccgggtgtgtggcaacat
                                                                                                                                                                                                                                              2 (bases 1 to 4112)
Li,Q.-z., Shi,J.-D., Cruz,P., Echenrode,S., Ruan,Q.-G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l (bases 1 to 4112)
Li,Q.-2., Ruan,Q.-G., Eckenrode,S., Shi,J.-D., Cruz,P., and She,J.-X.
                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A new gene which is highly expressed in NOD mice spleen
Unpublished
                                                           Indels
                                   Length
                                               5.2e-112;
                                                             ;
0
                                   DB 6;
                         gggccttttaccgcagctacaccaccagctg 399
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
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/note="50E12"
                                                          392; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete cds.
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
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                                   Query Match
                                               Local
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ORGANISM
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                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                      Song, H., Gao, G., Peng, Y., Ren, S., Chen, Z. and Han, Z.
A novel gene expressed in human hypothalamus
Unpublished
2 (bases 1 to 1429)
Song, H., Gao, G., Peng, Y., Ren, S., Chen, Z. and Han, Z.
Direct Submission
Submitted (12-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, China
Location/Qualifiers
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68.7%; Pred. No. 1.2e-103;
1ive 0; Mismatches 239;
                                                                                                                                                                                                                                        /organism="Homo sapiens"
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1. 1429
                                                                                                                                                                                                                                                                                                                                                    /product="HT015 protein"
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                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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5869 bp mRNA linear ROD 07-NOV-2001 Mus musculus mitochondrial carrier-like protein mRNA, complete cds; AF361699
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PLRGINWMMMAGPHAMYFACYENMKRTLNDVFSHQGNSHLANGILKAFVWSWEALL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5869)
Li,Q., Eckenrode,S., Wang,C., Ruan,Q., Shi,J., McIndoe,R.A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-MAR-2001) Department of Pathology, Immunology and Laboratory Sciences, University of Florida, 1600 SW Archer Road, Room D6-15, Gainesville, FL 32610, USA
99t999gtgaccgcctatttccgagggtgcaggccagagtaatttaccagatccctcc 717
                                                                                                                                                                          541 accccactggacgtttgcaaaacactgctcaacacccaggagtccttggc---tttgaac 597
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                                                                             aacccaagctcccacgtcctctctggagcttgcgcaggagctgtagctgccgcagccaca
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/organism="Mus musculus"
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Matches 393;

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2611 CTGGCCGCAGCTGCCCCCCCCCGCTGGACGTCTGCAAAACCCTCCTCAACACGCAGGAG 2670
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2851 CTTACAAAGAGGCAGCTGGAG 2871

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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                       1736436 seqs, 858457221 residues
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Human polynucleoti	Human transport pr	Human uncoupling p	Human polynucleoti	Human ORFX ORF398	Human dene express	Human secreted pro	cDNA sequence #574	Human mitochondria
SUMMAKIES	æ	Query	ID	*	AA160661	AAF27733	AAC90457	AAI58875	AAC74843	AAZ15876	AAS03906	AAS62787	AAH22162
			DB	1	22	22	21	22	21	20	22	24	22
			Length		1294	1322	1336	1316	1418	710	2502	2037	664
			Match		100.0	100.0	100.0	0.66	87.1	80.1	72.2	69.7	65.2
			Score		798	798	798	790	695	639	576	556	520
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AAK69779 AAK73320 AAK73320 AAF66156 AAC71189 AAC77189 AAC9220 AAC9220 AAC9220 AAC9220 AAC6452 AAC6452 AAC6452 AAC6452 AAC66452 AAC7177 AAC77173 AAC77173 AAC77173 AAC93357 AAC93357 AAC93357 AAC93357	AAR80493 AAR91764 AAR91764 AAR93200 AAR83356 AAS31106 ALIGNMENT	t entry) de SEQ ID NO 4650. immunosuppressant; cy system; neuropathy; nson's disease; Hunti; 1 sclerosis; Shy-Drag mbolytic; drug screen O-US34263. S-0552317. S-0558042. S-0650312. S-0650312. S-0653450. S-0662191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed
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Zhang J;
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Yang Y,
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100.0%; Pred. No. 2.5e-245;
ive 0; Mismatches 0;
                                                            Ma Y,
Xue AJ,
                                                                                                                                                                        useful
                                                                            Wehrman T, Xu C, Xue AJ
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                    Claim 1; SEQ ID NO 4650; 10078pp; English.
                                                                                                                                                                       Novel nucleic acids and polypeptides, us
such as central nervous system injuries
                                                              Asundi V, Chen R,
29-NOV-2000; 2000US-0727344
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P-PSDB; AAM41505.
                                                            Liu C, A
Wang Z, W
Zhou P,
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ses 798; Conserv
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                                                            Tang YT,
Wang J, w
Zhao QA,
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The present invention provides the protein and coding sequences for 43 movel human transport proteins (designated TPPTs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative
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neurological disorder; cardiovascular disorder; reproductive disorder;
immune disorder; cancer; ss.
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accccactggacgtttgcaaaacactgctcaacacccaggagtccttggetttgaactca
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u DAM, Au-Young J, Patterson
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                                                                                                                                                                                                                                                                                                                                                                         Human transport protein TPPT-33 coding sequence.
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the diagnosis, prevention and
1 the immune, reproductive and
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99US-0148177.
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P-PSDB; AAB60113.
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10-AUG-1999;
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28-OCT-1999;
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08-JUL-1999;
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     Length 1322;
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                Indels
     ; DB 22;
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                Mismatches
     Score 798;
Pred. No. 2
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antirheumatic; antiproliferative; cardiant; vasotropic; cerebroproctective; neuroprotective, antibacterial; opthalmological; gastrointestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding uncoupling proteins. The nucleotide sequences may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
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Zhang J;
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Yang Y,
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u C, Xue AJ,
Drmanac RT;
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Wehrman T, Xu
Goodrich R,
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Wang Z,
Zhou P,
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19-JUL-2000; 2
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19-OCT-2000;
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the encoded polypeptides (AAMS642-FAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and C.N.S. disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415
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                                                                                      disorders
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                                                                                      treating
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                                                                                   polypeptides, us
system injuries
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                                                                                                                                                                                                                                 invention relates to
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2001-442253/47
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Matches 793; Conserv
                          P-PSDB; AAM39719
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
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                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF398 polynucleotide sequence SEQ ID NO:795
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                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                              AAC74843 standard; cDNA; 1418
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antiinflammatory; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, astuma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinfiammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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        atgcagagtctacagcctgacccagctgccgctatcgcaatgtgttggaggcctctgg
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antidiabetic; hypotensive; dermatological; immunosuppressive;
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                                                                                                                                                                                                                                                                                      Sequence 1418 BP; 353 A; 400 C; 368 G; 297 T; 0 other;
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Pred. No. 2.9e-212;
0; Mismatches 0;
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89.6%;
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Best Local Similarity 89.6
Matches 798; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancercus state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancercus, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypetides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the
                                                          caggccagagtaatttaccagatcccctccacagccatcgcatggtctgtgtatgagttc 1017
898 gctagtgccttcaggacggtatatcaagtaggtggggtgacgcctatttccgaggggtg 957
                                                                                                                                                                                                                                                                                                                             detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                           caggccagagtaatttaccagatccctccacagccatcgcatggtctgtgtatgagttc
                                                                                                                                                                                                                                                                                                               Human; gene; gene expression product; diagnosis; therapy; probe;
                                                                                 Human gene expression product cDNA sequence SEQ ID NO:3345.
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Escobedo J, Garcia PD, Garcia V, Giese K, Innis M;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
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                                                                                                                                                                                        AAZ15876 standard; cDNA; 710
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98US-0072910.
98US-0075954.
98US-0080114.
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31-MAR-1998;
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diagnosis, prognosis and management of colorectal cancer, breast can and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.
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                                                                            Sequence 710 BP; 186 A; 187 C; 183 G; 154 T; 0 other;
                                                                                                                                     80.1%; Score 639; DB 20; I 100.0%; Pred. No. 1.9e-194;
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Matches 639; Conserv
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Sequence 2037 BP; 475 A; 522 C; 524 G; 515 T; 1 other;
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                                                                                                                                                                                                                                             Forty one nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
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                                                                                                                                                                                                                                                                                                           Disclosure; Page 460-461; 518pp; English.
                                                                                                                                                                     Ruben SM, Rosen CA;
                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                          26-SEP-2000; 2000WO-US26324
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Best Local Similarity 100.
Matches 576; Conservative
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            WO200123598-A1.
                                                                                                                                                                     Komatsoulis G,
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Human secreted protein; hyperproliferative disorder; autoimmune disorder;
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                                                                                                                                                                                                                                                                                                       encoding the secreted proteins. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and infectious disorders (e.g. hepalitis). The polynucleotide sequences of the invention are also useful in gene therapy. AAS62214-AAS62838 represent the cDNA sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RJ;
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                                tccttggctttgaactcacacattacaggacatatcacaggcatggctagtgccttcagg
                                                                                                                                   acggtatatetcaagtaggtgggtgaccgcctatttccgaggggtgcagggccagagtaatt
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Pred. No. 1.3e-167;
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        Similarity
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                                                                                                New human mitochondrial solute carrier (hMSC) protein isomer and its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein, designated hMSC-homologue, which is expressed in human hypophysis. Also described are methods for the preparation and detection of hMSC-homologue protein and nucleotide sequences. The present sequence encodes hMSC-homologue, as given in the present
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                                                                                                                                                                                                                                              Sequence 997 BP; 240 A; 261 C; 242 G; 254 T; 0 other;
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           STATE HUMAN GENE GROUP.
                                                                                                                                    Claim 1; Page 17-18 (disclosure); 22pp; Chinese.
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  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                   RESULT 11
                                                                                    AAK73320
                    a
                                                                                                                  AMEA9951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inscrting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases especially cancer metastases of haematopoietic-derived cells. AAK64703 co AAK87694 represent invention. AAK54942 to AAK87650 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                               Disclosure; SEQ ID NO 24591; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.7%; Score 508; DB 22; Length 27960; 99.8%; Pred. No. 1.3e-151; ive 0; Mismatches 0; Indels 1;
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                                                                                  Ruben SM;
                                                  (HUMA-) HUMAN GENOME SCI INC.
11-DEC-2000; 2000US-0254097. 05-JAN-2001; 2001US-0259678.
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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cartivity, and can be used in AMM81210 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. ARK54912 to AAK8056 and AAM82169
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                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
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                                                20000S-0250391.
20000S-0251030.
20000S-0251988.
20000S-0256719.
20000S-0256719.
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemia condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic claseases. ABI99913 and ABI99914 represent POR primers for a mouse ischaemic condition related sequence,
                                                                                                                                                                    21323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                 21144 ggagtccttggctttgaactcacacattacaggacatatcacaggcatggctagtgcttt
                                                                                                                                                      ggagtccttggctttgaactcacacattacaggacatatcacaggcatggctagtgcctt
                                                                   caggacggtatatcaagtaggtggggtgaccgcctatttccgaggggtgcaggccagagt
                                                                                                                                      aatttaccagatcccctccacagccatcgcatggtctgtgtatgagttcttcaaatacct
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                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                          ABI99871 standard; cDNA; 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-034733/04.
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Length 483;

Score 417.8; DB 24; Pred. No. 1.4e-123;

52.4%; 93.2%;

Best Local Similarity

Query Match

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 Gaps
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mson G, Drmanac R;
                   165 gttaaaaaagacattgagtgatgtaatccaccctgggggcaatagccatattgccaatgg
                                                                                                     caagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgtacgggc
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                                                                                                                                                      465 cccccagagacggtacaacccaagctcccacgtcctctggagcttgcgcaggagctgt
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                                      15 gttaaaaaagacattgagtgacgtaatccacccagggggggaatagccatattgccaatgg
                                                                                                                                                                                     gaacgttcctttccaagccattcacttcatgacctatgaattcctgcaggagcactttaa
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Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences –
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Leshkowitiz
 Indels
                                                                                                                                                                                                                                                                                                            585 cttggctttgaactcacacattacaggacatatcacaggcatggctagt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tic; gene therapy; colon cancer;
lung cancer; cancer detection; s
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Mismatches
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Kennedy GC,
Dickson M,
LW, Strache
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99US-0142311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams LT, Escobeco c, Reinhard C, Randazzo F, F
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Conservative
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HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-091805/10
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cancer; lunc
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Matches 437;
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                                                                    The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed ques correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of theraphes and preventions. The polynucleotides and preventive interventions. The polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antidiamemic; gene therapy; cancer; prolliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardlovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 401 BP; 100 A; 104 C; 120 G; 76 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.3e-115;
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100.0%; Pred. No. 2.3e-115;
11ve 0; Mismatches 0;
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Claim 9; Page 818; 1046pp; English.
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antithenumatory; antibacerial; antiviral; antithenumatic; antithyroid; and antianemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovasular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria, autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
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neurodegenerative disorders and cardiovascular disease
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68.7%; Pred. No. 6.7e-110;
iive 0; Mismatches 240;
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                                                                                                                                                                               thrombosis; contraceptive; ss.
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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The invention relates to a novel human mitochondrial solute carrier protein, hMSC-0 (AAB60658), and cDNA encoding it (AAF59920). hMSC-0 is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-0 proteins and nucleic acids, and the detection of hMSC-0 proteins and nucleic acids, in a sample. The present sequence represents cDNA encoding hMSC-0.
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                                                                                                                                                                                                                                                                                                                                                                                                                               ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg
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                                                                                                                                                                                                                                                                          1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg
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                                                                                                                                                                                              Length 1305;
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                                                                                                                                         Sequence 1305 BP; 292 A; 388 C; 363 G; 262 T; 0 other;
                                                                                                                                                                                            Score 365.6; DB 22;
Pred. No. 1.3e-106;
); Mismatches 239;
                                                                                                                                                                                                                                    .,
                                                                                                                                                                                            Query Match
Best Local Similarity 68.7%;
Matches 533; Conservative
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Sequence 1, Appliance 151, Appliance 151, Appliance 151, Appliance 151, Appliance 151, Appliance 151, Appliance 160, Appliance 1, Appli

Sequence 6, Appli Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli

us-09-870-113-7.rni

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database

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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
APPLICANT: and Rex Michael Brennan
TITLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                         US-09-132-652-1

US-08-997-080-151

US-08-997-852-151

US-09-095-855-151

US-09-324-542-151

US-08-630-915A-33

US-08-943-731-640

US-07-945-283-3

US-08-203-389-1

US-08-179-738-1

US-08-628-145-1
                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-179-738-6
US-08-628-145-6
US-08-179-738-4
US-08-628-145-4
      US-08-896-449A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807-
FILING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                5215881-1
5215881-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDUIW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 9, Application US/09068140A; Patent No. 6281409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1311 base pairs
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; STRAIN: Ben Alder
US-09-068-140A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: unknown unknown
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                                                            TYPE: nucleic acid
STRANDEDNESS: unkno
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(without alignments)
1076.653 Million cell updates/sec
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Sequence 3, Appli
Sequence 45, Appl
Patent No. 5223423
Sequence 374, App
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 262, App
Sequence 1, Appli
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                                                                                                                                                                                                                                                                                                                                                                                            l atgcagagtctacagcctga......agtggagggctggcaagtga 798
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Sequence
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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US-08-891-298-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383533 segs, 122816752 residues
                                                                                                                                                                                                           September 28, 2002, 07:55:43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                              nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
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798
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Match Length
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81.2 81.2 36.6 36.6 36 36 35

Result No.

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                                                                                                                                                                     287 CAATGGGTCTCGGTGCAGGACCAGCTCACGCAGTGTATTCTCCCGTTTACGAGATGTGTA 346
                                                                                                                                                                                                                                                                                                                                                                        agaggatgcagatgtacaactcaccataccaccgggtgacagactgtgtacgggcagtgt 349
                                                                         50 aggccctctggaggattataagaacggaggcctatggaggcccatgaggggctgaacg 109
                                                                                                                                                                                                                                                  347 AGGAGACTITITCICATG-----GTGATCCGAGCAATTCCGGTGCGCACTTT 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caggagctgtagctgccgcagccacaaccccactggacgtttgcaaaacactgctcaaca 574
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                                      Gaps
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                                      24;
Length 1311;
                                    0; Mismatches 248; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan TITLE OF INVENTION: Blackcurrant Promoters and Ger NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: ADDRESSE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
Score 81.2; DB 4;
Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/EP96/04807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/068,140P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-068-140A-14
; Sequence 14, Application US/09068140A
patent No. 6281409
; GENERAL INFORMATION:
10.2%;
50.2%;
                                  Matches 274; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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COUNTRY: USA
ZIP: 19406-0939
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cccagg 580
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 Query Match
                     Best Local
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3391 AAGCCCTTGGGTCGATACTGAAAGTTGAAGGTCCCGCCGGACTTTACCGTGGCATTGGTG 3450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3622 AGAGGTTGCAGTTGCAGAGCAGTCCGTACAAGGGTGTTGTTGATTGCGTGAGGAGGGTGT 3681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3742 CCCCGTTTACGGCCGTTCACTTCGCCACATATGAAGCCACGAAGAAAGGGTTGTTGGAGG 3801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 aggccctctggaggattataagaacggaggcctatggaggcccatgagggggctgaacg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 ttcctttccaagccattcacttcatgacctatgaattcctgcaggagcactttaacccc 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 aaaagacattgagtgatgtaatccacctggggggcaatagccatattgccaatggtgcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81.2; DB 4;
Pred. No. 2.2e-16;
0; Mismatches 248;
FILING DATE: NO. 6281409ember 4, 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 61, Application US/08933750C Patent No. 5932442
                                          NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C7/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%;
50.2%;
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 5150 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Ribes nigrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.2
Best Local Similarity 50.2
Matches 274; Conservative
                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                         TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                       unknown
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3922 GCCAAG 3927
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US-08-933-750C-61
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
   Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61:
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                                         Shah, Purvi
Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                          IBM Compatible
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LENGTH: 1594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 51.59
Watches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LIBRARY: SPLNNOT02
; CLONE: 207452
US-09-234-613-61
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                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                              Palo Alto
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                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                 94304
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                                                                                                                                                                                                                                CITY: Palc
STATE: CA
                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                                          APPLICANT:
                                                                                                                                                                                                                                                                    COUNTRY:
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4.6%; Score 36.6; DB 2; Length 1594;
Best Local Similarity 51.5%; Pred. No. 0.046;
Matches 84; Conservative 0; Mismatches 79; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1080 CTCGTATGAATTCTTCTGTAATGTCTTCCACTGCATGAACAGG 1122
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                                                                                                               APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
MUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/933,750C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     September 23, 1997
               Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice
Yue, Henry
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Sequence 61, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PF
TELECOMOUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LIBRARY: SPLNNOT02; CLONE: 207452
US-08-933-750C-61
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                            CITY: Palo
STATE: CA
COUNTRY: U
                                                                                                                                                                                                                                                                                                                      94304
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1020 CTTCAAGGGCCTGTCCCCCAGCTTGCTGAAGGCTGCCCTCTCCACAGGCTTCATGTTCTT 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36.6; DB 3; Length 1594;
Pred. No. 0.046;
0; Mismatches 79; Indels 0
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APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: COTLEY, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                  E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0356 US
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US-08-933-750C-68
Sequence 68, Application US/08933750C
FACTOR NO. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FLING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
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386 acaccacccagetgaccatgaacgttcetttccaagccattcacttcatgacctatgaat 445
                                                              836 GGGCCCCCACTGCCCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAACTATGAGC 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 ggaggcccatgagggggctgaacgtcacagcaacaggcgcagggcctgcccacgcccttt 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 3; Length 1643;
                                                                                                                                      896 TGGTGAAGAGCTGGCTCAATGGGCTCAGGCCGAAGGACCCAGACTTC 941
                                                                                                         446 tectgeaggageaetttaaeeeeeagagaeggtaeaaeeeaagete 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Blilings, Lucy J.
REFERENCE/DOCKET NUMBER: 96,749
REFERENCE/DOCKET NUMBER: PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/933,750
                                                                                                                                                                                                                                                            Sequence 68, Application US/09234613
Patent No. 6132973
                                                                                                                                                                                                                                                                                                                           Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.58;
                                                                                                                                                                                                                                                                                                                                                                                           Shah, Purvi
Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1643 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 44.09
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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CLONE: 724157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 PO CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94304
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                                                                                                                                                                                                                                   US-09-234-613-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 255; Indels
               APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 2;
Pred. No. 0.073;
                                                                                                                                                                       E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 44.0%;
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
Shah, Purvi
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: SYNOOAT01;
CLONE: 724157
US-08-933-750C-68
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                                                                                                                                                                                         STREET: 3174 Por
CITY: Palo Alto
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                94304
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206 atagccatattgccaatggtgcggccgggtgtgtgggcaacattacttcatgatgcagcca
                                                                                                                                                                      656 CTGACCTCTACGCACCCATGGTGGCTGGCGCGCTGGCCCGCTTGGGCCACCGTGACTGTGA
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                                                                                              502 ACTICACIGCCIAIGACCAACIGAAGGCCIICCIGIGIGGICGAGCCC-----IGACCI
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29,768
FR: 30472/114 IMMU
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NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMM TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFRONE: (703)836-9300 TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDUIW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-232-463-14/C
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                                                                                                                                             Gaps
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                                                                                                 Score 35; DB 1; Length 7218;
Pred. No. 0.33;
                                                                                              4.4%; Score 35, 4.1%; Pred. No. 0.33; 4.1%; Pred. No. 10.33; 1183; Mismatches 148; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NR/An-
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ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-009
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08937466 Patent No. 5846779
                                                                                          Query Match
Best Local Similarity 4.1%; Prec
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                , CLONE: PTZ9pt-F1s
US-08-232-463-14
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STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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IMMEDIATE SOURCE:
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ZIP: 94010
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double

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STRANDEDNESS:
             ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-09-172-528-5
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                                                                                                              Query Match
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                                                                                                                                                      244 acattacttcatgatgcagccatgaaccctgcggaagtggtcaagcagaggatgcagatg 303
                                                                                                                                                                                                                               304 tacaactcaccataccaccgggtgacagactgtgtacgggcagtgtggcaaaatgaaggg 363
                                                                                                                                                                                                                                                                 390 CAGAGCGTGCAGTACCGCGGTGTGCTGGGTACCATCCTGACTATGGTGCGCACAGAGGGT 449
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                                                                                                                                                                                       330 ACTITICCCCIGGACACCGCCAAGGICCGICIGCAGAICCAAGGGGAGAACCCAGGGGCT 389
                                                                                                                Gaps
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0
                                                                         Length 1777;
                                                                         Score 32.4; DB 2; Length 1 Pred. No. 1.1; 0; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T97-009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.509-172-528-5
; Sequence 5, Application US/09172528
; Patent No. 5952469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
                                                                                              44.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                           Query Match
Best Local Similarity 44.13
Matches 135; Conservative
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STATE: CALIFORNIA
COUNTRY: USA
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   CDNA
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APPLICANT: Zhang,
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 ; MOLECULE TYPE:
US-08-937-466-5
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APPLICATION NUMBER: US/09/318,199
                                                                                                               Score 32.4; DB 2;
Pred. No. 1.1;
0; Mismatches 171;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
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Patent No. 6025469
GENERAL INFORMATION:
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                       4.18;
44.18;
                                                                                                                                           Best Local Similarity 44.1
Matches 135; Conservative
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linear
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INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                          Gaps
                                                                                                                                                     Length 1777;
                                                                                                                                                 Query Match 4.1%; Score 32.4; DB 3; Length 1
Best Local Similarity 44.1%; Pred. No. 1.1;
Matches 135; Conservative 0; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC CUMPACATE OPERATING SYSTEM: PC-DOS/MS-DOS GOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: ILLLSBOROUGH STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
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APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09503579
Patent No. 6248561
GENERAL INFORMATION:
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T9:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
LENGTH: 1777 base pairs
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APPLICATION NUMBER: US
FILING DATE:
               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
WOLECULE TYPE: CDNA
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                                                                                                                                                                                                          Score 32.4; DB 4; Length 1 Pred. No. 1.1; 0; Mismatches 171; Indels
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75 DENISE DRIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: G
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: T9-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                          Query Match 4.1%;
Best Local Similarity 44.1%;
Matches 135; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                   / TOPOLOGY: Linear
// MOLECULE TYPE: CDNA
US-09-503-579-5
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544 ccactg 549
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US-09-318-199-3
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                                                                                                                                                                                         Length 1949;
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APPLICATION NUMBER: US/09/172,528
                                                                                                                                                                                         Score 32.4; DB 2;
Pred. No. 1.2;
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APPLICANT: Zhang, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROGH
STATE: CALIFORNIA
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/CDCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09172528
Patent No. 5952469
SEQUENCE CHARACTERISTICS:
LENGTH: 1949 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-937-466-3
                                                                                                                                                                                     Query Match
Best Local Similarity 44.1%;
Matches 135; Conservative
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14.1%; Pred. No. 1.2;
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Patent No. 6025469;
GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS
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TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1949 base pairs
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 44.19
Matches 135; Conservative
                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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STATE: CALTECT
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APPLICATION NUMBER: US/08/937,466
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APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
AITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09503579 Patent No. 6248561 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1949 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 135; Conservative
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MEDIUM TYPE: Floppy of
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; MOLECULE TYPE: CDNA
US-09-318-199-3
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Job time: 11239 sec
36,627
R: T97-009
                    REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                   TELEPHONE: (650) 343-4341
TELEFRAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                Query Match 4.18;
Best Local Similarity 44.18;
                                                                                                                                                             LENGTH: 1949 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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     REGISTRATION NUMBER:
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BI794616 ic92e02.y BG295496 602392826 AV704087 AV704087 BG964218 602828996 AA061624 mj90h11.r BF078769 229199 MA BE913718 601669072

AL563845 AL563845 AJ397503 AJ397503

AA234031 Z149D10.r B1185580 UNL-P-FN-BF916224 CM2-UT011 AF015710 Mus muscu B1045863 MR3-FN020 B1041453 B7041453 AW211366 U080b07.y B1339456 384426 MA B1304641 AR063B091 A1743110 wg87d01.x W35634 md15a04.r1 BF076673 226290 MA AKO06155 Mus muscu AI208913 9960a03.x BMS5880 523415 MA BG982657 IL5-CN006 BC055067 nac99a08.

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0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NHW GC Library." 1 others
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11 HGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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B1254253 GI:14806485
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM11277 row: i column: 07
High quality sequence stop: 825.
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                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:5114190"
/clone=lib="NIH_MGC_12"
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Pred. No. 6.1e-160;
0; Mismatches 0;
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233 c
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99.88;
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Simpson,A.J.
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1 (Dases 1 to 966)

1 (Dases 1 to 966)

1 (Mases 1 to 966)

1 National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

1 Contact: Robert Strausberg, Ph.D.

2 Email: cgapbs-rémail.nih.gov

7 Tissue Procurement: DCTD/Prp/Gazdar

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: L.CM/LS1 Incyte Collumn: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung, Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscribt II RT (Life Technologies). Note: this is a
NIH MGC Library ...
277 c 248 g 193 t
                  EST 27-FEB-2001
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               BG331197 986 bp mRNA linear EST 27-FE 602431907F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4549801
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Pred. No. 1.3e-159;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_18"
                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 587.
Location/Qualifiers
1. .986
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                                                                              BG331197.1 GI:13137635
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                                                mRNA sequence.
BG331197
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Best Local (
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/note="Organ: placenta_normal; Vector: puc18; Site_1: Smal : Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-GN0338-230201-558-a01&t3=2001-02-23&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence start: 18
High quality sequence stop: 575.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
601
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                                                                                                                                                                                                                                                                                                                                                                                                                482 ACCGCCTATTTCCGACGGGTGCAGGCCAGAGTAATTTACCAGATCCCCTCCACAGCCATC
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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/db_xref="taxon:9606"
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BI057218.1 GI:14464748
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Mutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
El (bases I to 927)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lonpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG972351 927 bp mRNA linear EST 12-JUN-2001
602841302F1 NCI_CGAP_KId14 Mus musculus cDNA clone IMAGE:4975441
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                                                             Gaps
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                                                                                                                                  283 gtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgtacgg
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                                                            Indels
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                                   10;
                                  Score 532.2; DB 10
Pred. No. 4.8e-144;
                                                          0; Mismatches
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                                   66.78;
99.38;
                                                         Matches 545; Conservative
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BG972351
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Mus musculus
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DEFINITION
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KEYWORDS
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908 bp mRNA linear EST 07-MAY-2001 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803681 5',
                                                                                                                                                                                  Site_1: NotI;
Imer: Oligo dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="FVB/N"
/db_xref="taxon:10090"
/clone="laMGE:4975441"
/clone=lib=Nor1_GCAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCWV-SPORT6; Site_1: No: Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                      210 ccatattgccaatggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaa 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 ccctgcggaagtggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgac 329
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Pred. No. 1.6e-139;
0; Mismatches 45;
02
                                                                      /organism="Mus musculus"
                  quality sequence stop: 812
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:13962975
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92.4%;
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29 Sep

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Bonaldo, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
blate: LLAMA1294 row: j column: 20
High quality sequence start: 7
High quality sequence stop: 809.

1. 855
                                                                                                              BI412175 855 bp mRNA linear EST 14-AUG-2001 602965377F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5120755 5',
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 855)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 GAGAATCATGAGGACAGAGGCCTGTGGAGGCCCATGCGGGGTGCTGAACGTCACAGCAA 205
                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 atgcagagtctacagcctgacccag-ctgcccgctatcgcaatgtgttggaggcctctg
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                       823
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Pred. No. 7.6e-133;
0; Mismatches 80;
         783 AATCACTAAAAGGCAAGAAGAAGAGGGGGGGGCTGGCAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="CZECH II"
/db_xref="taxon:10090"
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87.9%;
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                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                      Confect: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov
Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
column: 10
Plate: Libral0699 row: o column: 10
Plate: Libral0699 row: o column: 10
High quality sequence stop: 878.

Location/Qualifiers

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1. 908
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 9.8e-137;
0; Mismatches 1;
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Best Local Similarity 98.8%;
Matches 574; Conservative
                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                       AUTHORS
TITLE
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COMMENT
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Query Match 59.3
Best Local Similarity 90.8
Matches 515; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
E 1 (bases 1 to 808)
S NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: GapAbs-rémail.nih.gov
Tissue Procurement: Jeffery Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10903 row: f column: 20
High quality sequence stop: 696.

Location/Qualifiers

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                             414 tttccaagccattcacttcatgacctatgaattcctgcaggagcactttaacccccagag
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/strain="FVB/N"
/db_xref="taxon:10090"
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         566
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Soares Rattus sp. cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 25-MAY-2000
                                                                                   /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Murinae;
                                                                                                                                                                                                                                                                                             462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtagetgeegecacacaaccecactggaegtttgeaaaacactgeteaacacecaggag 582
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Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
                                                                                                                                                                                                                                                                                                                                                                  gtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgtacgg
                                                                                                                                                                                                                                                                                                                                                                                                  GTCAAGCAGAGGATGCAGATGTACAACTCGCCGTACCACCGCGTGACAGACTGTTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atgaacgttcctttccaagccattcacttcatgacctatgaattcctgcaggagcacttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aacccccagagacggtacaacccaagctcccacgtcctctggagcttgcgcaggagct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 ACGGTCTATCAAGTAGGCGGGGTGACTGCTTACTTCCGAGGGGTGCAGGCCAGAGTCATT
                                                                                                                                                                                                                                                             5;
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                             Length 808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                         Score 473; DB 10;
Pred. No. 9.8e-127;
); Mismatches 50;
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KGICM3 5, end, mRNA sequence.
AW915209
AW915209.1 GI:8080897
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Rodentia;
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                                                                                                                                                                                                                           59.3%;
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Euteleostomi; Sus.

TITLE

COMMENT

FEATURES

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                  Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                   Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pcMv SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 174 c 146 g 103 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 agaggatgcagatgtacaactcaccataccaccgggtgacagactgtgtacgggcagtgt 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggcaaaatgaaggggcggggccttttaccgcagctacaccaccagctgaccatgaacg 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGCAAAACGAAGGGGCCGGGGCCTTTTACCGCAGCTACACACCCAGCTCACCATGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 ttcctttccaagccattcacttcatgacctatgaattcctgcaggagcactttaacccc 469
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                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 563)
                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 470.6; DB 10
Pred. No. 4.2e-126;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC_2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 71 row: A column: 23
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                     FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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PCR PRimers
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95.3%;
                                                                                                                                                                                           Contact: Smith TPL
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                  Rat
                                                                                                                                                                                                                                                    /organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGICM53"
/clone="RGICM53"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
a 157 c 131 g 110 t
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                  (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541 accccactggacgtttgcaaaacactgctcaacacccaggagtccttggctttgaactca
                                        Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Tel: (301)-888-3529
Fax: (301)-888-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gccattcacttcatgacctatgaattcctgcaggagcactttaacccccagagacggtac
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                  EST
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 472.6; DB 9;
Pred. No. 1.1e-126;
0; Mismatches 34;
                  Rat
              Genome Project: Generation of a
 Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      59.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 93.5
Matches 493; Conservative
              Rat Genome
Gene Index
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/db_xref="taxon:9606"
/clone="InAGE:2871968"
/clone=lib="NOILCGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH108"
/note="Organ: lung; Vector: pT773D-pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo.

Soares and M. Fatima Bonaldo.

2 others
                                                                                                                                                                        AW341177 581 bp mRNA linear EST 31-JAN-2000 xz95e05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871968 3' similar to TR:Q94638 Q94638 MITOCHONDRIAL SOLUTE CARRIER. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing Center information can be
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                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 581)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 TCCCCTCCACAGCCATCGCGTGTCTGTGTATGAGTTCTTCAAATACCTGATCACTAAAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 agtggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgt 338
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High quality sequence stop: 369.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome (Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Best Local Similarity 97.5%; Pred. No. 2.4e-125;
Matches 474; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                  AW341177.1 GI:6837803
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Unpublished (1997)
                                                                                                                                                                                                                                      seguence
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TITLE
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BF143133 830 bp mRNA linear EST 24-OCT-2000 601788025F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015758 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arzayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LiAM9262 row: a column: 07
High quality sequence stop: 607.
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                                                                                                                                                                                                                                                                                               aatttaccagatcccctccacagccatcgcatggtctgtgtatgagttcttcaaatacct 758
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                                                                                                                         275 CTTTAACCCCCAGAGAGGGTACAACCCAAGCTCCCACGTCCTCTCTGGAGCTTGCGCAGG 334
ctttaacccccagagacggtacaacccaagctcccacgtcctctctggagcttgcgcagg
                                                                                                                                                                      519 agetgtagetgeegeageeaaaceeeaetggaegtttgeaaaacaetgeteaaeaceea
                                                                                                                                                                                                                                                                      579 ggagtccttggctttgaactcacacattacaggacatatcacaggcatggctagtgcctt
                                                                                                                                                                                                                                                                                                                                                                   639 caggacggtatatcaagtaggtggggtgacgcctatttccgaggggtgcaggccagagt
                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:4015758"
/clone_lib="NCI_CGAP_Lu30"
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BACKWARD: GTTTTCCCAGTCACGACG
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Best Local Similarity 94.7%;
Matches 469; Conservative
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.a. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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1 (bases 1 to 578)
Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Gasas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertaa, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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                                                                                                522
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                                                 gtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgtacgg 342
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                                                                                                                                                                                                                                                                                                              643 acggtatatcaagtaggtgggtgaccgcctatttccgaggggtgcaggccagagtaatt 702
                                                                                                                                                                                                                                                                                                                                                                                                     taccagatccctccacagccatcgcatggtctgtgtatgagttcttcaaatacctaatc 762
                                                                         9
                           Gaps
                                                           aaccccagagacggtacaacccaagctcccacgtcctctggagcttgcgcaggagct
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 Length 830;
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536233 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BM483098.1 GI:18533417
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PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4356
Fax: 402 762 4399
 DB 10;
             Pred. No. 4.4e-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actaaaaggcaagaagagtggagggctggcaagtga 798
                       0; Mismatches
56.8%; Score 453.6; 92.4%; Pred. No. 4.4
                    477; Conservative
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Contact: Smith TPL
           Similarity
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COMMENT
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1. .578

Corganism="Bos taurus"

Ab_xref="taxon:9913"

/clone_lib="MxRC 3B0v"

/tissue_type="pooled"

/lab_host="bH10B"

/note="vector: pcWV SPORT6; Site_1: Xbal; Site_2: Xhol;

Library made from pooled tissue from marrow, alveolar

macrophage, ovary, fetal semitendonosus muscle, and fetal

a 184 c 141 g 114 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 888)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccaagctcccacqtcctctctggagcttgcgcaggagctgtagctgcagcaacaacc 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGGGGGCCTTTTACCGCAGCTACACCACCCAGCTCACCATGAACGTTCCCTTCCAAGCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attcacttcatgacctatgaattcctgcaggagcactttaacccccagagacggtacaac 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATTCACTTCATGACCTACGAATTCCTGCAGGAGCACTTTAACCCCCAGAGACGGTACAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITACAGGACATATCACAGGCATGGCTAGTGCCTTCAGGACGGTGTATCAAGTAGGCGGG 360
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 453.4; DB 10;
Pred. No. 4.4e-121;
0; Mismatches 26;
Plate: 5 row: F column: 16
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/organism="Homo saplens"
/db_xref="taxon:9606"
/clone='Inacon:9606"
/clone='Inacon:9606"
/clone='Inacon:9606"
/clone='Inacon:9606"
/clone='Inacon:9606"
/clone='Inacon:9606"
/clone='Inacon:97130-pac (Pharmacia).with a modified
/note="vector: pT7130-pac (Pharmacia).with a modified
as a ubtracted library derived from NCI_CGAP_Sub6
as a tracer in a subtractive hybridization with a driver
comprising: the InAGE pool (NCI_CGAP_Kid3) pool 1 LLAM
3334-3337, 3682-383911, 145608-1456775, L505052-1502855;
/note="vector: pT733191, 1012-1305931, 1473691, 1520944-1522439
/note="vector: pT733191, NCI_CGAP_Pr22 pool 1 LLAM 3157-3182,
/note="vector: pT733191, NCI_CGAP_Pr22 pool 1 LLAM 2457-2459,
/note="vector: pT733191, NCI_CGAP_Pr22 pool 1 LLAM 2457-2459,
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/note="vector: pT733191, NCI_CGAP_Pr22 pool 1 LLAM 244-2659,
/note="vector: pT733191, NCI_CGAP_Pr22 pT733191, NCI_CGAP_Pr22 pool 1 LLAM 244-269,
/note="vector: pT733191, NCI_CGAP_Pr22 pool 1 LLAM 
                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov
The sequence contained an oligo-dT track that was present in the
Oligonucleotide that was used to prime the synthesis of first
strand CDNA and therefore this may represent a bonafide poly A
tail. CDNA Library Preparation: M.B. Soares Lab Clone distribution:
WIT-CGAP clone distribution information can be found through the
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 451)
                                                                                                                                                                                                        NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA-Yes.
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129 c 1
   GI:11600447
                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                         Tumor Gene Index
                                                                                             Homo sapiens
   BF515180.1
                                                              human.
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IMAGE:3082698 3', mRNA sequence.
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                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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      Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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045997 Onchocerca
ACC67971 Sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
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Larsson C., Suomalainen A.;
"Characterization of a novel human putative mitochondrial transporter
homologous to the yeast mitochondrial RNA splicing proteins 3 and 4";
FEBS Lett. 494:79-84(2001).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R., Larsson,C. and Suomalainen,A. Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing
                                                                                                                                                                                               ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q24"
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/protein_id="AAK49520.1"
/db_xref="G1:13926050"
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NTQESLALNSHITGHTTGMASAFRTVYQVGGVTAYFRGVQARVIXQIPSTAIAMSVYE
FFKYLITKRQEBMRAGK<sup>H</sup>
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Li.F., Nikali, K., Gregan, J., Leibiger, I., Leibiger, B., Schweyen, R., Larsson, C. and Suomalainen, A.
Direct Submission
Submitted (08-DEC-2000) Human Molecular Genetics, National Public Health Institute, Mennerheimintie 166, Helsinki 00300, Finland
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alternatively spliced"
/codon_start=1
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( Dases 1 to 1889)

Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R., Larsson,C. and Suomalainen,A.

Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing
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                        9 GTCTACAGCCTGACCCAGCTGCCCGCTATCGCATGTTTGGAGGCCCTCTGGAGGATTA
                                                                                taagaacggagggcctatggaggcccatgagggggctgaacgtcacagcaacaggcgcag
    gtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctggaggatta
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                /product="mitochondrial RNA splicing protein 3/4"
/function="putative mitochondrial solute carrier"
/function="putative mitochondrial solute carrier"
/function_id="CAC2796.1"
/translation="WaELEGRAGGYAGGPAAGPGRSPGESALLDGWLORGYGGAGGGE
AGACRPPVRQDPDSGPDYEALPAGATVTHMVAGAVAGILEHCVMYPIDCVKTRMOSLQ
                                                                                                                 PDPAARY RNVLEALMRIIRTEGLMRPMRGLNVTATGAGPAHALY FACYEKLKKTLSDVI
HPGGNSHIPAMGAAGCVATLLHDAANNHABEVVKQMWNY NSFYRVTDCYRAVWQNBCSAG
AFYRSYTTOLTMNVPECPA HHEWY TEFLQBHFNDQRRYN SSHVLSGACAGAVAAATTP
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Milliams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J., Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D., Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M., Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crain,B. Human genes and gene expression products
Patent: WO 0102568-A 1912 11-JAN-2001; CHIRON CORPORATION (US); HYSEQ, INC. (US)
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100.0%; Pred. No. 1.2e-80;
ive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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/gene="HMRS3/4"
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Mammalia; Eutheria; Primates;
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100.0%;
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Matches 225; Conservative
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/function="putative mitochondrial solute carrier"
/function="putative mitochondrial solute carrier"
/frotein_id="CAC27997.1"
/franslation="MNPRA7997.1"
/TMNVPFOALHFWYPETCBHFNPORRYNPSSHVLSGACAGAVAAAATPELDVCKTLLNT
QESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFK
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Butheria; Primates; Catarrhini; Hominidae; Homo
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Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
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Larsson C., Suomalainen A.;
"Characterization of a novel human putative mitochondrial transporter
homologous to the yeast mitochondrial RNA splicing proteins 3 and 4";
FEBS Lett. 494:79-84(2001).
                                                                                     ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
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                        Indels
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    Pred. No. 2.2e-64
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26-APR-2001 (Rel. 67, Last updated, Version 2)
                        Mismatches
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/gene="HMRS3/4"
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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at
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Direct Submission
Submitted (25-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Sep 26, 2001 this sequence version replaced gi:14280413.
During sequence assembly data is compared from overlapping clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggattataagaacggagggcctatggaggcccatgagggggctgaacgtcacagcaaca 120
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Catarrhini; Hominidae;
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Pred. No. 2.2e-64;
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findPhrapList
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JOURNAL
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Rattus norvegicus chromosome Rfl clone CH230-24M6, WORKING DRAFT
SEQUENCE, 33 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85540 ATGCAGAGTCTACAGCCTGACCCAGCTGCCCGCTATCGCAATGTTTGGAGGCCCTCTGG 85481
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/clone_lib="RPCI-11.1"
complement(7066. .7118)
/note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."
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100.0%; Pred. No. 4.2e-64;
ive 0; Mismatches 0; Indels
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                                                         /organism="Homo sapiens"
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Location/Qualifiers
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1 (bases 1 to 221062)
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Matches 225; Conservative
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Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, Manselwari, M., Mapua, P., Martin, R., Martindale, A., Martine, E., Massey, E., Mawhiney, E., Martin, R., Martindale, A., Martine, Martine, Martine, Martine, Martine, Martine, Martine, Martine, Martine, Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Moyren, N., Nguyen, J., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rutves, M., Rojas, A., Rolle, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, M., Mall, R., Wang, S., Warten, R., Washington, C., Wallianon, S., Warten, R., Washington, C., Walliams, G., Williamson, A., Wleczyk, R., Woden, S., Worley, K., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
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NOTE: This is a working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15627972.
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of 12736 bp in length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
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Worley, K.C.
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Unpublished
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4112 bp mRNA linear ROD 27-OCT-2001 mitochondrial solute carrier-like protein mRNA,
                                                                                                                                                                                                                                                                         (bases 1 to 4112)
Li,Q.-Z., Ruan,Q.-G., Eckenrode,S., Shi,J.-D., Cruz,P., Wang,C.-Y. and She,J.-X.
A new gene which is highly expressed in NOD mice spleen
                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
116. .1132
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93.8%; Pred. No. 1.6e-56;
ive 0; Mismatches 14;
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of 3838 b
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/translation="MELREGOVGNQAAGRRMDGDCRDGGCGSKDAGSEDYENLPTSAS
VSTHMTAGAMAGILEHSIMYPVDSVKTRMQSLNPDPKARYTSIYGALKRIMHTEGFWR
PLRGLNVMMMGAGPAHAMYFACYENWKRTLNDVFSHQGNSHLANGVAGSMATLLHDAV
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YEFLQEQVNPRRDYNPQSHIISGGLAGALAAAATTPLDVCKTLLNTQENMALSLANVS
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                                                                             Direct Submission
Submitted (20-JUL-2000) Pathology, University of Florida, 1600 SW
Archer Road, Rm. D6-15, Gainesville, FL 32610, USA
Location/Qualifiers
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/protein_id="AAL23859.1"
/db_xref="GI:16506178"
2 (bases 1 to 4112)
Li,Q.-Z., Shi,J.-D., Cruz,P., Echenrode,S., Ruan,Q.-G. and Wang,C.-Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.8%; Score 139.2; DB 10; Length 4112; 68.6%; Pred. No. 1.8e-35; ive 0; Mismatches 88; Indels 0;
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GRLSGMANAFRTVYQLNGLPATSKASRRVSSTRCPPPPFLGLSMSSSSTFSPSASWKI
ELHTKGRDHRIFS"
                                      PRI 17-APR-2000
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YSTHWTAGAMAGILEHSVWPYDDSVKTRWDSLESPPRAQYTSYTGALKKIMFTEGFWR
PLRGVNWMINGAGPHAMYFRCYENNKRTLNDYFHHGGNSHLANGIAGSMATLLHDAV
MNPAEVVKQRLQMYNSQHRSAISCIRTVWRFEGLGAFVRSYTTQLTMNIFPQSIHFIT
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                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1429)
                                                                                                                                                                                                                                                                                                        Song, H., Gao,G., Peng, Y., Ren, S., Chen, Z. and Han, Z.
Direct Submission
Submitted (12-JAN-2000) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 Argcagacrrragarccagarcccaaagcccagracacaagrarcracgagcccrcaag 320
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                          nr.zz390b 1429 bp mRNA linear PR:
Homo sapiens HT015 protein (HT015) mRNA, complete cds.
AF223466
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A novel gene expressed in human hypothalamus
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1. .1429
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/protein_id="AAF64141.1"
/db_xref="G1:7578783"
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/db_xref="taxon:9606"
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RATURD.

RAT
ALUMYSER 163205 bp DNA linear HTG 20-DEC-2001 Rattus norvegicus clone CH230-84G11, *** SEQUENCING IN PROGRESS
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On Dec 20, 2001 this sequence version replaced gi:16901901.
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae;
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Web site: http://www.hqsc.bcm.tmc.edu/
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                                                                                                                                                                                         GI:17973175
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Mammalia; Eutheria;
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Rattus norvegicus
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
           Estimated insert size: 120308; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation
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Best Local Similarity 87.4%;
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http://wchanning.bwh.harvard.edu:9088/hpcgg/jsp/hpcgg/Sequence/mous
       HTG 06-FEB-2002
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (absel to 1b.).
Grills,G., Li,L., Montgomery, K.T., Brown, W.A., Chiu,D., Decker,J., Fusina,M., Haider,A., Keller,A., Perera,A., Shim,C., Thomas,E., High Throughput Mouse Sequencing Rucherlapati,R.
ACI08878 191702 bp DNA linear HTG 06-FEB-200
Mus musculus clone RP23-256H24 strain C57BL6/J, *** SEQUENCING IN
PROGRESS ***, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-FEB-2002) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: agarose-FP - N/A Quality coverage: 5.6 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                2 (Dases I to 191702)
Grills,G., Li,L., Montgomery,K.T., Brown,W.A., Chiu,D., Decker
Fusina,M., Haider,A., Keller,A., Perera,A., Shim,C., Thomas,E.
Zencheck,W., Xi,C., Juels,P. and Kucherlapati,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Feb 6, 2002 this sequence version replaced gi:18464039.
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Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 1008
*Consensus quality: 187211 at least 020
*Consensus quality: 185727 at least 030
*Consensus quality: 183181 at least 030
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 191382 - sum-of-contigs
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Center Code: HPGC
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/evidence=not_experimental
/product="mitochondrial carrier-like protein"
/protein_id="AAL27990.1"
/db_xref="G1:1675528"
/translation="MELRRGGVGNQAAGRRMDGDCRDGGCGSKDAGSEDYENLPTSAS
VSTHWTAGAMAGILEHSINYPVDSVKTRMQSLNPDPKARYTSIYGALKRIMHTEGFWR
PLRGLNVMMMGAGPAHAMYFACYENMKRTLNDVFSHQGNSHLANGILKAFVWSWEALL
                                                                                                                 AF361699 5869 bp mRNA linear ROD 07-NOV-2001 Mus musculus mitochondrial carrier-like protein mRNA, complete cds; nuclear gene for mitochondrial product.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5869)
Li,Q., Eckenrode,S., Wang,C., Ruan,Q., Shi,J., McIndoe,R.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                 carrier protein gene is up-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-MAR-2001) Department of Pathology, Immunology and Laboratory Sciences, University of Florida, 1600 SW Archer Road, Room D6-15, Gainesville, FL 32610, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 5869)
Li,Q., Eckenrode,S., Wang,C., Ruan,Q., Shi,J., McIndoe,R.A. and
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/map="between D14Mit124 and D14Mit236"
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Db 13898 GATGTAATCCACCCGGGGCAATAGCCATATGCCAATGGT 13939
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Pred. No. 1.5e-25;
0; Mismatches 72;
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A novel mouse mitochondrial of from young to adult NOD mice Unpublished
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/note="MCLP"
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Best Local Similarity 68.0%;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagata, T. and Ishii, Y.
                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 191702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 483;
                          188416: contig of 2003 bp in length 188416: contig of 2003 bp in length 189584: contig of l148 bp in 1190648: contig of unknown length 190648: contig of unknown length
                                                                                                                                                                                                                                                                                                         360 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD 106463 AATGACGTTTTCAGCCACCAAGGAAACAGCCATCTAGCTAATGGT 106507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                         contig of 1044 bp in length
gap of unknown length
contig of 1034 bp in length.
                                                                                                                                                                          in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 agtgatgtaatccaccctggggggcaatagccatattgccaatggt 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I (sites)
Ishikawa,K., Asal,S., Takahashi,Y., Nagata,T.
Ishikawa,K., Asal,S., Takahashi,Y., Nagata,T.
Method for examining ischemic conditions
Patent: WO 0188188-A 1009 22-NOV-2001;
School Juridical Person Nihon University (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 105.2; DB 6;
Pred. No. 3.5e-24;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                  38.5%; Score 109.8; DB 2; ilarity 68.0%; Pred. No. 2.6e-25; Conservative 0; Mismatches 72;
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unknown
of 1367
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AX306258
AX306258.1 GI:17645513
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                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="RP23-256H24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483 bp
                contig
gap of
contig
gap of
                                                                                                                                                                                            Location/Qualifiers
 gap of
                                                                                                                                                                                                                                          /strain="C57BL6/J"
                                                                                                                                          190648:
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Best Local Similarity 93.2%;
Matches 110; Conservative (
                                                                                                                                                                           191702:
                                                                                                                                                                                                                                                                                        'sex="male"
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186394
186414
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189605
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                               83976
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                                                                                                                                                                                                                                                                                                                                                                                                  153;
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ORIGIN
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VERSION
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AX306258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
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LOCUS

165 gttaaaaaagacattgagtgatgtaatccaccctgggggcaatagccatattgccaatgg 224

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AFZ16674 108765 bp DNA linear HTG 02-JUN-2001
Homo sapiens chromosome 8 clone RP1-158P13 map 8p, WORKING DRAFT
SEGORECE, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I chases 1 to 108765)
Schilhabel, M. B., Baumart, C., Blechschmidt, K., Dette, M., Jahn, N., Lehmann, R., Menzel, U., Polley, A., Reichwald, K., Schudy, A., Siddiqui, R., Taudien, S., Wen, G., Schlegelberger, B., Siebert, R., Chromosome 8 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2. (bases 1 to 108765)
Pooley, A., Wen,G., Baumgart,C., Dette,M., Jahn,N., Schilhabel,M., Men,G., Baumgart,C., Dette,M., Jahn,N., Schilhabel,M., Direct Submission
Direct Submission
Biotechnology, Beutenbergstrasse 11, Jona 07745, Germany on Jun 2, 2001 this sequence version replaced 91:8151796.
Center: Insitute of Molecular Biotechnology
Center code: IMB
* consists of 16 conties. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; 100% of reads
Sequencing vector: M13; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 87772 bases at least 040
Consensus quality: 95159 bases at least 030
Consensus quality: 100612 bases at least 030
Consensus quality: 100612 bases at least 020
Quality coverage: 3,95 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1101: contig of 1101 bp in length 1201: gap of unknown length 21239: contig of 19938 bp in length 21239: gap of unknown length 36201: contig of 14962 bp in length 35301: gap of unknown length 47101: contig of 10800 bp in length 47201: gap of unknown length 67201: gap of unknown length 56806: contig of 9605 bp in length
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unknown length
of 8338 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
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of 8177 bp in l
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                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT.
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73621:
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56907
65084
65184
73522
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1500 others
                                  gap of unknown length
contig of 2870 bp in length
gap of unknown length
contig of 2796 bp in length
                                                                                                      bp in length
                                                                                                                  gap of unknown length contig of 2142 bp in length
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contig of 1441 bp in length
gap of unknown length
                                                                                                                                                                                      contig of 3246 bp in length gap of unknown length
bp in length
                                                                                         length
                                                                                                                                                                                                                                                                                                         /clone="RP1-158P13"
25034 c 24818 g 28459 t
                                                                                                                                                                                    101563: contig of 3246
101663: gap of unknown
108765: contig of 7102
                                                                                                       contig of 1965
                                                                                                                                                                                                                                        1. .108765
/organism="Homo sapiens"
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/map="8p"
                                                                                                                                                                                                                                .ocation/Qualifiers
                                                                                          gap of
                                                                                                                                                                     98218
98318
101564
101664
                      81424
86504
86604
89474
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96677
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ORIGIN
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DD 68859 ATGCAGAGTTTGAGTCCCAGATCCCAAGTACACAGTGTCTACGGAGCCCTCAAG, 68918 Gaps 1 atycagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg 60 Query Match 36.8%; Score 105; DB 2; Length 108765; Best Local Similarity 66.7%; Pred. No. 9.8e-24; Matches 150; Conservative 0; Mismatches 75; Indels 0;

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181 agtgatgtaatccaccctgggggcaatagccatattgccaatggt 225

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Search completed: September 28, 2002, 07:58:26 Job time: 14827 sec

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September 28, 2002, 08:06:20; Search time 664.31 Seconds (without alignments) 736.585 Million cell updates/sec
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4.5
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1736436 seqs, 858457221 residues
GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                    OM nucleic - nucleic search, using sw model
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length: 2000000000
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285
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Perfect score:
Sequence:
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Maximum DB s
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human ORFX ORF398	Human polynucleoti	Human transport pr	Human uncoupling p	Novel human polynu	Human polynucleoti	Human secreted pro	Human immune/haema	Human immune/haema
SUMMARIES	ID		AA160661	AAF27733	AAC90457	AAF66156	AA158875	AAS03906	AAK69779	AAK73320
	DB	21	22	22	21	22	22	22	22	22
	Query Match Length DB	1418	1294	1322	1336	401	1316	2502	27960	27960
œ	Query Match	100.0	98.2	98.2	98.2	95.8	95.4	78.9	78.9	78.9
	Score	285	280	280	280	273	272	225	225	225
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immune/ha polynucle mitochoud omstochoud immune/ha full-leng full-leng full-leng full-leng opolynucle opoky onex onex omstochoud oms	Human secreted pro Human secreted pro CDNA sequence #574 Drosophila melanog Human ORFX ORF2246 Aspergillus oryzae Arabidopsis thalia Arabidopsis thalia Blackcurrant pRIB7 Blackcurrant pRIB7 Drosophila melanog	Human mitochondria Human mitochondria Human uncoupling p Human ORFX ORF2547 Human Clone cg4399 Human Clone cg4399 Probe for DNA enco
AAK5867 AAK5217 AAK5217 AAC77192 AAC1302 AAC1302 AAC1302 AAC1302 AAC9286 AAK9286 AAK9487 AAK9489 AAK9489 AAK9489 AAK9489		
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339 1902 17105 17105 2562 300 700 1913 842 842 1814 1819 1989 1989 1989 1989 1989 1989	1758 1758 2037 2137 6712 6712 673 1371 1371 1311 5150 6326	111 154 156 166 5
0 44 44 44 44 64 66 66 66 66 66 66 66 66	32.1 20.1 12.0 12.0 11.0 11.8 11.8 11.4 11.4 11.4	111111111111111111111111111111111111111
174 129.6 128 128 128 121 107.6 105.2 105.2 105.2 105.3 105.3 105.4 105.4 107.6 105.4 107.6 107.	99 99 99 99 99 99 99 99 99 99 99 99 99	32 32 32 31.8 31.8 31.8
1100 1100 1100 1100 1100 1100 1100 110	33333333333333333333333333333333333333	39 444 444 443 45 45
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ALIGNMENTS

AAC74843 standard; cDNA; 1418 BP.

AAC74843

W Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
w unincerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
w anticonvulsant; Osteopathic; coagulant; vasotropic; antidiabetic;
w hypotensive; dermatological; immunosuppressive; antiinflammatory;
w antiviral; antibacterial; antifungal; antitheumatic; antithyroid;
antiviral; antibacterial; antifungal; antitheumatic; antithyroid;
antiviral; gene therapy; cancer; proliferative disorder; hypertension;
neurodegenerative disorder; osteoarthritis; graft vs host disease;
neurodegenerative disorder; osteoarthritis; graft vs host disease;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
hone danage; cartilage damage; antiinflammatory disease; coagulation;
w thrombosis; contraceptive; ss. Human ORFX ORF398 polynucleotide sequence SEQ ID NO:795. 08-FEB-2001 (first entry) AAC74843;

Homo sapiens.

WO200058473-A2.

05-OCT-2000

31-MAR-2000; 2000WO-US08621.

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AAI60661;
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                                                                                                                                                                                                                                                                                  which represent the human ORRY open reading frames 1 to 3161. The ORRY sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipachinsonian; noctropic; neuroprotective; osteopathic; anticonvulsant; antiarthitic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidianaetory; antibacterial; antivital; antifungal; antithermatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating nucleic acids can be used to express ORRY proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                        AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                   Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgtggaggccctctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 gcaacattacttcatgatgcagccatgaacctgcggaaggctga 285
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                                                                                                                                                                                                                                           Claim 5; Page 853-854; 5507pp; English.
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            99US-0127607.
99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                               Leach M;
                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                          WPI; 2000-602362/57.
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                                                                                                                                                         P-PSDB; AAB40634
                                                                                                              Shimkets RA,
                           02-APR-1999;
05-APR-1999;
                                                       30-MAR-2000;
               31-MAR-1999;
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
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                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Yang Y,
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100.0%; Pred. No. 4.5e-85;
iive 0; Mismatches 0;
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Xue AJ,
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Drmanac RT;
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                                                   Human polynucleotide SEQ ID NO 4650.
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Wehrman T, Xu
Goodrich R,
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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20000S-0662191.
20000S-0693036.
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Matches 280; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
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Wang 2,
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                                                                                                                                                                                                                                                 Leukaemia; ss
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09-JUL-2000;
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14-SEP-2000;
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22-OCT-2001
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AAI60661 standard; cDNA; 1294 BP

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              aggattataagaacggagggcctatggaggcccatgaggggggctgaacgtcacagcaaca
                                                     ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaaagacattg
                                                                                                                                                                                                                                                                              Human; uncoupling protein; immunosuppressive; antiarthritic;
                                                                                                                                         gcaacattacttcatgatgcagccatgaaccctgcggaag
                                                                                                                                                                                                                                                            Human uncoupling protein cDNA #6
                                                                                                                                                                                                  AAC90457 standard; cDNA; 1336
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                                                                                                                                                                                                                                                        Human; transport protein; TPPT; transport disorder; metabolic disorder;
neurological disorder; cardiovascular disorder; reproductive disorder;
immune disorder; cancer; ss.
1074 AGGATTATAAGAAGGAGGCCTATGGAGGCCCATGAGGGGGTGTGAACGTCACAGCAACA 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide with a human transport protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular systems -
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                                                                                        895
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                                       agtgatgtaatccaccctggggggcaatagccatattgccaatggtgcggccgggtgtgtg
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Patterson (
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                                                                                                                    894 GCAACATTACTTCATGATGCAGCCATGAACCCTGCGGAAG 855
                                                                                                                                                                                                                                     Human transport protein TPPT-33 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillman JL, Tang YT
Lu DAM, Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 160; 165pp; English
                                                                                                                                                                          AAF27733 standard; cDNA; 1322
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99US-0149357.
99US-0162287.
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                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders such as cancer
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MR, Azimzai Y,
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28-OCT-1999;
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antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; neuroprotective, antibacterial; opthalmological; gastrointestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Uncoupling proteins and nucleic acid sequences encoding them, usefu: for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0142821.
99US-0149448.
99US-0164751.
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                                                                                                                                                 infertility; ss
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                                                                                                                                                                                                                              Homo sapiens
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18-AUG-1999;
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Length 1322;

Score 280; DB 22; Pred. No. 4.6e-85;

98.2%; Scur 100.0%; Pre 0;

Matches 280; Conservative

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Query Match Best Local Similarity

Mismatches

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                                                                                                 316
                                                                                                                   180
                                                                                                                                                                 Gaps
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or
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        Length 1336;
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       Score 280; DB 21;
Pred. No. 4.6e-85;
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Kennedy GC, Pot D, La
Dickson M, Labat I,
LW, Strache-Crain B;
                                                                                                                                                                                                                                                                                                                               tic; gene therapy; colon cancer;
lung cancer; cancer detection; s
                                                                                                                                                                                                                                                                                                             Novel human polynucleotide, SEQ ID NO: 1912
                         Mismatches
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98.2%; Sur-
100.0%; Pre
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99US-0142311.
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Reinhard C, Randazzo F,
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, Drmanac S,
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Kita D, Garcia V, Jones
                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-091805/10.
                Similarity
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breast cancer; lung
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02-JUL-1999;
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       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                   67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                  their gene products are used as genetic or biochemical markers (e.g. blood or tissues) that will detect the earliest changes along the carchnogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions threat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                   gtctacagcctgacccagctgcccgctatcgcaatgtgttggaggcctctggaggatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       taagaacggaggcctatggaggcccatgagggggctgaacgtcacagcaacaggcgcag
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                                                                                                                                                                                                                                                                                                             Length 401;
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                                                                                                                                                                                                                            Sequence 401 BP; 100 A; 104 C; 120 G; 76 T; 1 other;
  antisense oligonucleotides can be generated. The
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                                                                                                                                                                                                                                                                                                          Score 273; DB 22;
Pred. No. 6.5e-83;
                                                                                                                                                                                                                                                                                          95.8%; Sco...
100.0%; Pred. No. co...
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2000US-052317.
2000US-0598042.
2000US-0653450.
200US-0653450.
200US-0653450.
200US-0653450.
200US-063450.
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                                                                                                                                                                                                                                                                                                          Query Match 95.8
Best Local Similarity 100.
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200153312-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 - SEP - 2000;
19 - OCT - 2000;
29 - NOV - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein; autoimmune disorder; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; bacterial infection; viral infection; ss; fungal infection; coular disorder; wound healing; tissue regeneration; epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 ggcgcatggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg
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      Ren F, W
Zhang J;
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      Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1316 BP; 335 A; 364 C; 337 G; 280 T; 0 other;
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                                                                     Drmanac RT;
                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1078; 10078pp; English.
                                                                                                                                                                                                                                                                           such as central nervous system injuries
   Asundi V, Chen R,
Wehrman T, Xu C,
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                                                                     Goodrich R,
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Matches 275; Conservative
                                                                                                                                       WPI; 2001-442253/47.
Tang YT, Liu C, 1
Wang J, Wang 2, 1
Zhao QA, Zhou P,
                                                                                                                                                                          P-PSDB; AAM39719
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AAS03906
      SO X X C C C C C C C C X D X X D D X X D D D X X D D X X D D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D
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Sequences AAS03873-AAS03922 represent isolated nucleic acid molecules and pcR primers of the invention. acid of the invention. Secreted proteins and their related nucleic acids can be used in the diagnosis of or susceptibility to a pathological condition by determining the presence or absence of a mutation in a nucleic acid or the presence or amount of expression of a secreted protein. The sequences are used to prevent, tract or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The antibodies to the polypeptides can also be used in alleviating symptoms associated with disorders and in diagnostic immunoasys e.g. radioinmunoasysy or enzyme linked immunosorbent assays (ELISA). The disorders include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. carebras is nersex, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Albeimer's disease, infections caused by meteria, viruses and fungiand ocular disorders e.g. corner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacteria, viruses and fungl and ocular disorders e.g. corneal infection The peptides can also be used to aid wound healing and epithelial cell proliferation, to help prevent skin againg due to sunburn, to maintain organs before transplantation, to regenerate tissues, in chemotaxis and as a food additive or preservative to alter storage capabilities.
                                                                                                                                                                                                                                                                                                                                       Forty one nucleic acid molecules encoding human secreted proteins, useful the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 374
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100.0%; Pred. No. 3.4e-66;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 460-461; 518pp; English
                                                                                                                                                                                                                                         Rosen CA;
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                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                  26-SEP-2000; 2000WO-US26324.
                                                                                                                                                          99US-0155807
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                                                                                                                                                                                                                                       Komatsoulis G, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.99
Best Local Similarity 100.
Matches 225; Conservative
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                                     WO200123598-A1
  Homo sapiens.
                                                                                                                                                          27-SEP-1999;
                                                                             05-APR-2001
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2000US-0237040.
2000US-0239935.
2000US-0239937.
2000US-0240960.
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                                                                                                                                      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24591
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                            (first entry)
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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                         06-NOV-2001
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2000US-0226279
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2000US-0229509.
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2000US-0230437.
2000US-0230438.
2000US-0231242.
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2000US-0232080
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19-MAY-2000; 2
07-JUN-2000; 2
28-JUN-2000; 2
07-JUL-2000; 2
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11-JUL-2000; 2
14-JUL-2000; 2
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18-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
23-AUG-2000; 2
33-AUG-2000; 3
                                          Homo sapiens.
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17-MAR-2000;
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
crample, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
cappenent the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
colynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK84921 to AAK84950 and AAM82169.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27960 BP; 7998 A; 5835 C; 6583 G; 7544 T; 0 other;
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                         20000S-0251869.
20000S-0251989.
20000S-0251990.
20000S-0254097.
20010S-0259678.
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11-DEC-2000;
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PR 27-SEP-2000; 2000US-025834.

PR 29-SEP-2000; 2000US-025834.

PR 29-SEP-2000; 2000US-025834.

PR 29-SEP-2000; 2000US-025836.

PR 20-CCT-2000; 2000US-0237039.

PR 20-CCT-2000; 2000US-023703.

PR 20-CCT-2000; 2000US-0237039.

PR 20-CCT-2000; 2000US-024180.

PR 20-CCT-2000; 2000US-02418
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) activity, and can be used in gene therapy and vaccine production. (1) activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and proteins and polynucleotides may be used in the prevention, diagnosis and example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome expression by rectifying mutations or deletions in a patient's genome cappelement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic related diseases, especially cancer metastases of haematopoietic derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK84942 to AAK860 and AAM82169
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                                                                                                                                                                              Disclosure; SEQ ID NO 28132; 3071pp + Sequence Listing; English.
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100.0%; Pred. No. 9.8e-66;
tive 0; Mismatches 0;
                                   Ruben SM;
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(HUMA-) HUMAN GENOME SCI INC
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                                   Barash SC,
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                                   Rosen CA,
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29-SEP-2000;	PR 02-OCT-2000; 2000US-0236802. PR 02-OCT-2000; 2000US-0237037. PR 02-OCT-2000; 2000US-0237038. PR 02-OCT-2000; 2000US-0237040. PR 02-OCT-2000; 2000US-0237040.	13-0CT-2000; 20-0CT-2000; 20-0CT-2000;	20-OCT-2000; 20-OCT-2000;	20-OCT-2000; 20-OCT-2000;	20-0C1-2000; 20-0CT-2000; 01-NOV-2000;	08-NOV-2000; 08-NOV-2000;	08-NOV-2000; 08-NOV-2000;	08-NOV-2000; 08-NOV-2000;	08-NOV-2000; 08-NOV-2000;	08-NOV-2000; 08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000; 08-NOV-2000;	08-NOV-2000; 17-NOV-2000;	17-NOV-2000; 17-NOV-2000;	17 - NOV - 2000;	17 - NOV - 2000; 17 - NOV - 2000;	17-NOV-2000;	17-NOV-2000; 17-NOV-2000;	17-NOV-2000; 17-NOV-2000;	17-NOV-2000; 17-NOV-2000;	17-NOV-2000; 17-NOV-2000;	17 - NOV - 2000;	17-NOV-2000;	01-DEC-2000;	05-DEC-2000;	05-DEC-2000; 06-DEC-2000;	08-DEC-2000; 08-DEC-2000;	08-DEC-2000;	08-DEC-2000;	11-DEC-2000; 05-JAN-2001;	PA (HUMA-) HUMAN GENOME SCI INC.	PI Rosen CA, Barash SC, Ruben SM;	DR WPI; 2001-483426/52. DR P-PSDB; AAM85891. XX
17-JAN-2001; 2001WO-US01354.	31-JAN-2000; 2000US-0179065. 04-FEB-2000; 2000US-0180628. 24-FEB-2000; 2000US-0184664. 02-MAR-2000; 2000US-0186350. 16-MAR-2000; 2000US-0186374.	-MAR-2000; -APR-2000; -MAY-2000;	07-JUN-2000; 2000US-0209467. 28-JUN-2000; 2000US-0214886.	-JUN-2000; -JUL-2000; -JHL-2000;	-JUL-2000;	4-JUL-2000; 6-JUL-2000;	6-JUL-2000; 4-AUG-2000;	-AUG-2000; -AUG-2000;	4-AUG-2000; 4-AUG-2000;	-AUG-2000; -AUG-2000;	-AUG-2000;	-AUG-2000;	AUG-2000;	- AUG - 2000; - AUG - 2000;	-AUG-2000; -AUG-2000;	-AUG-2000;	SEP-2000;	-SEP-2000;	-SEP-2000;	-SEP-2000; -SEP-2000;	SEP-2000; SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000; SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	EP-2000; EP-2000; EP-2000;

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20-JUN-2000;
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                                                                                AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) anno acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic related diseases, especially cancers and cancer metastases of haematopoletic actived cells. AAK64703 to AAK87694 represent human immune/maematopoletic antigen genomic sequences from the present invention. AAK84921 to AAK84950 and AAM82169 represent invention.
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 aggattataagaacggagggcctatggaggcccatgagggggctgaacgtcacagcaaca 120
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                                                                                                                                                                                                                                                                                                                                                                                        Length 339;
                                                          Claim 1; SEQ ID NO 3732; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                               Sequence 339 BP; 86 A; 84 C; 101 G; 64 T; 4 other;
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Pred. No. 3.3e-49;
1; Mismatches 8;
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94.9%;
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27-APR-2000; 2000US-0560875.
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Best Local Similarity 94.9
Matches 188; Conservative
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                                metastasis -
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encoded polypeptides (AAM)8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity issue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAW80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggtgcagggccatgccatgccatgtattttgcctgctatgaaaacatgaaaaggacttta 1457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to polynucleotides (AAK51456-AAK53435) and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                 ι C, Cας
· Wang ZW;
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Chen R,
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Pred. No. 9.6e-34;
0; Mismatches 94;
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                                                                                                                                                                                                                                                         Zhou P,
                                                                                                                                                                                                                                                   , Asundi V, Zhou
Zhang J, Ren F,
, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in diagnosis and gene therapy
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Wang D, Wang J, Zh
Yang Y, Wejhrman T,
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                          2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0598075
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Best Local Similarity 66.4
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-476283/51
                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAM79039
                                19-JUL-2000;
01-SEP-2000;
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20-OCT-2000;
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Zhao QA,
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immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic;
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                                                                                                                                                                                                                                                          The invention relates to a novel human mitochondrial solute carrier protein, hMSC-o (AAB60658), and cDNA encoding it (AAF59920). hMSC-o is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-o proteins and nucleic acids, and the detection of hMSC-o proteins and nucleic acids in a sample. The present sequence represents cDNA encoding hMSC-o.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, open reading frame, ORFX, detection; cytostatic; hepatotropic, vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
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                                                                                                                                                                                                                    New human mitochondrion solute carrier protein and its nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                         232 aaaatcatgcggaccgaaggcttctggaggcccttgcgaggcgtcaacgtcatgatcatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 ggtgcagggccggcccatgccatgtattttgcctgctatgaaaacatgaaaaggacttta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtg
         carrier protein; hMSC-o; hypothalamus;
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0; Mismatches
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                                                                                                    17-MAR-2000; 2000CN-0114958
                                                                                                                         2000CN-0114958
          solute
                    preparation; detection; ss
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                                                                                                                                                                  Xiao H;
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nes 185; Conservative
         Human mitochondrial
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                                                                                                                                                                  Gao X,
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                                                                                                                         17-MAR-2000;
                                         Homo sapiens
                                                           CN1269409-A.
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Matches
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatorropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coapulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotension to, or preventing or treating the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy cetors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, astahma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, noctural haemoglobinizia, antiinflammatory disease; to enhance
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                                                                                            hypertension;
                                                                              antianaemic; gene therapy; cancer; proliferative disorder; hypertension, neurodegenerative disorder; osteoathriits; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 atgcagagttttgagtccagatcccaaagcccagtacacaagtatctacggagccctcaag 315
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hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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66.1%; Pred. No. 3.2e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis; contraceptive; ss
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99US-0127728.
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P-PSDB; AAB42980.
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05-APR-1999;
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                                                                                                                                                                                                                                                                              Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polynucleotide and the polynucleotide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheinmer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one
                     ggcgcagggcctgcccacgcctttattttgcctgctacgaaaagttaaaaaagacattg 180
                                                                           aaaatcatgcggaccgaaggcttctggaggcccttgcgaggcgtcaacgtcatgatcatg 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                           376 ggtgcagggccagcccatgccatgtattttgcctgctatgaaaacatgaaaaggacttta
                                                                 Liu C, Asundi V, Chen R, Ma Y;
Xu C, Xue AJ, Yang Y, Zhang J;
                                                                                                                                   gecaccetgetecacgatgeggtaatgaatecageagaag
                                                                                                             gcaacattacttcatgatgcagccatgaaccctgcggaag
                                                                                                                                                                                                                                                           Human bone marrow cDNA, SEQ ID NO: 301.
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Zhou P, Drmanac RT;
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                                                                                                                                                                                         AAH90057 standard; cDNA; 2562
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0653450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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14-SEP-2000;
19-OCT-2000;
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Zhao QA,
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of
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or more types of cancer. The polynucleotide and polypeptide can used as nutritional sources or supplements and in the screening chemical compounds as potential drugs.
                                                                                                                                                                                                            0;
                                                                                                                                                              44.9%; Score 128; DB 22; Length 2562; 66.1%; Pred. No. 3.8e-33; Live 0; Mismatches 95; Indels 0
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brcia PD, Garcia V, Giese K, Innis MA;
sam A, Kennedy GC, Kita D, Labat I;
hwwitz D, Pot D, Randazzo F, Reinhard
Sudduth-Klinger J, Williams LT;
                                                                                            652 T; 0 other,
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Garcia V, Glesc.
Kennedy GC, Kita D, Labr
                                                                                          Sequence 2562 BP; 623 A; 660 C; 627 G;
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98US-0072910.
98US-0075954.
98US-0080114.
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                                                                                                                                                                                         Best Local Similarity
Matches 185; Conserv
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28-JAN-1998;
24-FEB-1998;
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03-APR-1998;
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                                                                                                                                                                   Query Match
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Claim 1; Page 774; 2479pp; English.
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The colf the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, ampping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, constride and lung cancer. The polynucleotides can also be used to screen for nortified and lung cancer. peptide analogues and antagonists.

Sequence 300 BP; 83 A; 76 C; 79 G; 62 T; 0 other;

ó 0; Gaps Query Match 42.5%; Score 121; DB 20; Length 300; Best Local Similarity 100.0%; Pred. No. 3.6e-31; Matches 121; Conservative 0; Mismatches 0; Indels (g ò

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Search completed: September 28, 2002, 08:06:28 Job time: 11583 sec

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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                     APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan TITLE OF INVENTION: Blackcurrant Promoters and Genes NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                       E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: No. 6381409ember 4, 1996
ATTORNEY/ACENT INFORMATION:
NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 base pairs
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CITY: King of Prussia
STATE: PA
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US-09-068-140A-9
                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                           4444666666666666
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STRANDEDNESS:
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 0000000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                  US-09-068-140A-9
RESULT
                                                              ; Search time 182.06 Seconds
(without alignments)
384.519 Million cell updates/sec
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                                                                                                                        1 atgcagagtctacagcctga......tgaaccctgcggaaggctga 285
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-068-140A-14
US-08-913-750C-68
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US-08-630-915A-33
US-08-630-915A-33
US-08-630-915A-33
US-08-630-915A-33
US-08-026-138E-6
US-08-026-138E-6
US-08-026-138E-6
US-08-026-138E-6
US-08-162-9
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                                                                                                                                                                      383533 seqs, 122816752 residues
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                                                               September 28, 2002, 07:55:54
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Maximum Match 100%
Listing first 45 summaries
                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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US-08-724-394A-21
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US-08-724-394A-21
US-08-724-394A-21
US-08-724-394A-21
US-08-724-394A-21
US-08-972-631-1
US-08-972-631-1
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US-08-972-631-1
US-08-972-631-1
US-08-972-631-1
US-09-225-170-1
US-09-37-466-5
US-09-37-466-5
US-09-172-528-5
US-09-173-528-5
US-09-173-538-5
US-09-173-538-5
US-09-503-579-5
                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                              ; Sequence 9, Application US/09068140A
; Patent No. 6281409
; GENERAL INFORMATION:
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3391 AAGCCCTTGGGTCGATACTGAAAGTTGAAGGTCCCGCCGGACTTTACCGTGGCATTGGTG 3450
50 aggccctctggaggattataagaacggagggcctatggaggcccatgagggggctgaacg 109
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APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Nell C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FASLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.2%; Score 32; DB 2;
49.4%; Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0356 US
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FILING DATE: September 23, 1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                          US-08-933-750C-68
: Sequence 68, Application US/08933750C
: Patent No. 5932442
                                                                                                                                                                                                                                                                                                                                    Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                                                                                  3511 AGGAGACTTTTTCTCATG 3528
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SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 49.44
Matches 83; Conservative
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
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APPLICATION NUMBER:
FILING DATE:
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ADDRESSEE: Incyte Ph
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; CLONE: 724157
US-08-933-750C-68
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                                                    Gaps
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             Score 32.4; DB 4; Length 1311; Pred. No. 0.1;
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Pred. No. 0.19;
0; Mismatches 66; Indels 0
                                                  66; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan
TITLE OF INVENTION: Blackcurrant Promoters and Genes NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: NO. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dinner, Dara L. REGISTRATION NUMBER: 33,680 REFERENCE/DOCKET NUMBER: C70237 TELECOMUNICATION: 610-270-5017
                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09068140A Patent No. 6281409 GENERAL INFORMATION:
               11.4%;
52.2%;
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52.2%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 5150 base pairs
TYPE: nucleic acid
                           Best Local Similarity 52.2' Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 709 Swedeland
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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US-09-068-140A-14
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Best Local Similarity
Matches 72; Conserva
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             Query Match
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APPLICANT: BORRAN, No. 6309820h
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: KOWIKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1055 AGCACCAGTGGCCCGGGATGCCCATGAACTGGCGCGCAGTTCGAGGAACCCAGAC 1114
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      86 ggaggcccatgagggggctgaacgtcacagcaacagggcgcagggcctgcccacgcccttt 145
                                    70 agaacggaggcctatggaggcccatgagggggttgaacgtcacagcaacaggcgcaggg 129
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                                                                                                                    146 attttgcctgctacgaaaagttaaaaaagacattgagtgatgtaatcc 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSFWARE: PatentIn Release #1.0, Version #1.30
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29.6; DB 4;
Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                             ; Sequence 33, Application US/08630915A; Patent No. 6309820; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 86-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SED ID NO: 33:
SEQUENCE CHARACTERISTICS:
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51.5%;
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Matches 68; Conservative
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ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 cctgcccacgcc 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                    RESULT 5
US-08-630-915A-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                         86 ggaggcccatgagggggctgaacgtcacagcaacaggcgcagggcctgcccacgcccttt 145
482 CTACCCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAGGCACGAGGGCACCA 541
                                                                      26 ctgcccgctatcgcaatgtgttggaggccctctggaggattataagaacggagggcctat 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 32; DB 3; Length 1643; llarity 49.4%; Pred. No. 0.16; Conservative 0; Mismatches 85; Indels
                                                                                                                               146 attttgcctgctacgaaaagttaaaaaagacattgagtgatgtaatcc 193
                                                                                                                                                                        602 ACTICACTGCCTATGACCAACTGAAGGCCTTCCTGTGTGGTCGAGCCC 649
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lal, Preeti
APPLICANT: Lal, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: AU-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil J.
APPLICANT: COILEY, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette COMPUTER: IBM COMPALIDLE OPERATING SYSTEM: DOS SOFWWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                 Sequence 68, Application US/09234613 Patent No. 6132973 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNOOAT01
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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Best Local Similarity
Matches 83; Conserv
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE
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US-09-234-613-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%; Score 29; DB 1; Length 1747; ilarity 57.0%; Pred. No. 1.8; Conservative 0; Mismatches 40; Indels
                                                                                            APPLICANT: Freeman Jr., Robert M.
APPLICANT: Plutzky, Jorge
APPLICANT: Neel, Benjamin G.
TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                         ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,389
FILING DATE: 28-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 ctacgaaaagttaaaaaagacattgagtgatgt 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 AGAGTCTCAGCCAACCTGGTGATTTTGTGCTCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,141
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: US 07/721,112
FILING DATE: 26-UNN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: BIH92-05MA TELECOMMUNICATION INFORMATION:
                                         Sequence 1, Application US/08202389
Patent No. 5536636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1747 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA FEATURE:
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Best Local Similarity
Matches 53; Conserva
                                                                               GENERAL INFORMATION:
APPLICANT: Freeman
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                                                                                                                                                                                                                                                                                                                   CITY: Lexir
STATE: MA
COUNTRY: US
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US-08-202-389-1
RESULT 6
US-08-202-389-1
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US-09-457-708-1/c

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100 gggctgaacgtcacagcaacaggcgcagggcctgcccacgccctttattttgcctgctac 159
Sequence 1, Application US/09457708
Patent No. 6326483
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sampson, Julian R.
APPLICANT: Van Slegtenhorst, Marjon
APPLICANT: Halley, Dicky
TITLE OF INVENTION: Compositions and Methods Based U
TITLE OF INVENTION: Sclerosis-1 (TSC-1) Gene and Gene Product
NUMBER OF SEQUENCES. 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Patent No. 5502166
GENERAL INFORMATION:
MASAYOSHI MISHINA
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nishiohata Residence 1-107
STREET: 5214, Wishiohata-machi
CITY: Niigata-shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.2%; Score 29; DB 4; Length 8600; Best Local Similarity 58.8%; Pred. No. 3.8; Matches 50; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,708
                                                                                                                                                                                                                                                                                  E: Vinson & Elkins
1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRI331/42002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 gaaaagttaaaaaagacattgagtg 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639-6585
TELEFAX: (202) 639-6604
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 8600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Niigata-ken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                          STREET: 1455 Penr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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ZIP: 20004-1008
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US-08-026-138E-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                            STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-09-457-708-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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APPLICANT: Lipscombe, Diane
APPLICANT: Lipscombe, Stephanie
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
TITLE OF ILLING DATE: B1055/7000
CURRENT APPLICATION NUMBER: US/09/268,163B
CURRENT APPLICATION NUMBER: US 60/077,901
EARLIER APPLICATION NUMBER: US 60/077,901
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENTH: 7011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 ATTATCATAGATGAGCCCCCATGGATGCCCAGGATGGGGGGTGAGAGTCTGAGCA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 attataagaacggaggcctatggaggcccatgagggggctgaacgtcacagca 117
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Pred. No. 6.6;
0; Mismatches
                                                                                                                           APPLICATION NUMBER: JF 173155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JF 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JF 303878/1992
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             FILING DALL:
ATTORNEY/AGENT INFORMALL:
NAME: Hamburg, C. Bruce
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-4551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 966-2340
TELEPHONE: (212) 963-7733
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR AGE IN NO: 6:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 6:
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 39563/1992
FILING DATE: 26-FEB-1992
APPLICATION NUMBER: JP 173155/1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TITLE: NOVEL PROTEINS AND GENES; RELEVANT RESIDUES IN SEQ ID NO: US-08-026-138E-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-268-163-9/c

, Sequence 9, Application US/09268163B

; Patent No. 6553091

; GENERAL INFORMATION:
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            FILING DATE: 26-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.44
Matches 38; Conservative
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Best Local Similarity 54.3'
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE: brain PUBLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: lines
MOLECULE TYPE: CI
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 1..7008
US-09-268-163-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
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Sequence 6, Application US/08026138E
Sequence 6, Application US/08026138E
Sequence 6, Application US/08026138E
Sequence 6, Application US/08026138E
SEQUENCE NOT SEQUENCE:
TTILE OF INVENTION:
NUMBER OF SEQUENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.0%; Score 28.4; DB 1; Length 4368; llarity 70.4%; Pred. No. 4.5; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE: Drain
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROFIEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 17: FROM 1 to 4368
ZIP: 951
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS v.5
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IDM Compatible OPERATING SYSTEM: MS-DOS v.5
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                      PALLOR METLICATION DATE:

FILING DATE: 26-FEB-1992
APPLICATION NUMBER: JP 193155/1992
FILING DATE: 30-JUN-1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-4551
TELECHOMICATION INFORMATION:
TELECHOMICATION INFORMATION INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nishiohata Residence 1-107
STREET: 5214, Nishiohata-machi
CITY: Nilgata-shi
                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/026,138E FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/026,138E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Niigata-shi
STATE: Niigata-ken
COUNTRY: JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 38; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-026-138E-17
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267 gaaccctgcggaaggc 282
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Matches 60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-185-432-3/c
                                                                                                                              US-09-162-484-19
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1390 GAGGCGTCATTTTGGTATGATCGTAACGGATACCTGCGCGGCTACTGAACACGTCGTTCC 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1270 IGCIGGIGGITCGAACAACACGCCCCTGAAGIAGIAGIAGICGCGGIIIAGGIIIIICAA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 gaggeceatgagggggetgaacgteacageaacaggegeagggeetgeecacgeeettta 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 ttttgcctgctacgaaaagttaaaaaagacattgagtgatgtaatccaccctgggggcaa 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 tagecatattgccaatggtgcggccgggtgtgtgtggcaacattacttcatgatgcagccat 266
                                                                                                                                                                                                                                                                                                   APPLICANT: So, Maddalene
APPLICANT: Hwa, Vivian
APPLICANT: Hassif, Xavier
TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.8%; Score 28; DB 3; Length 2379;
46.4%; Pred. No. 4.6;
tive 0; Mismatches 105; Indels
                                                                                          ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,361E
FILING DATE: 02-OCT-1995
CLASSIFICATION: 536
                                                               227 cggccgggtgtgtggcaacattacttcatgatgcagccatgaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: No. 6121077nan, Kevin E
REGISTATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEPHONE: 312-913-0001
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               Sequence 5, Application US/08537361E Patent No. 6121037 GENERAL INFORMATION:
APPLICANT: Stojlijkovic, Igor
                                                                                                                                                                                                                                                                                Stojiljkovic, Igor
So, Magdalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..2376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 91; Conserva
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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GENERAL INFORMATION:
APPLICANT: Phillips, M. Ian
TILE OF INVENTION: ANTIEBNSE OLIGONUCLEOTIDE COMPOSITIONS TARGETED TO
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME MRNA AND METHODS OF USE
FILE REFERENCE: UFLA.087.VUELA087P
CURRENT APPLICATION NUMBER: 60/059,661
EARLIER APPLICATION NUMBER: 60/059,661
EARLIER APPLICATION NUMBER: 60/059,661
EARLIER FILING DATE: 1997-09-25
NUMBER OF SEQ ID NOS: 1997
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2989 ggccacatccagtatttcatgcagtacaaagacttgcctgtgacctttcgggagggcgc 3048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 goccaegecetttattttgeetgetacgaaaagttaaaaaagaeattgagtgatgtaate 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DELTEX PROTEINS, NUCLEIC ACIDS, AND ANTIHODIES, AND RELATED METHODS AND COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.7%; Score 27.6; DB 4; Length 3942; 52.6%; Pred. No. 8.2; tive 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Autsun, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLE:
TITLE OF INVENTION: DELTEX PROTEINS, NUCLE:
TITLE OF INVENTION: DELTEX PROTEINS, NUCLE:
TITLE OF INVENTION: DELTEX PROTEINS, STREETIS NUMBER OF SEQUENCES: 23
CORRESPONDEMES PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                   ; Sequence 19, Application US/09162484
; Patent No. 6248724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/08185432
; Patent No. 5750652
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-1994
Nr: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-162-484-19
1210 AATCACGCCGCTGGC 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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MEDIUM TYPE: Floppy
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SEQUENCE CHARACTERISTICS:
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US-08-475-844-8
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APPLICANT: Busseau, Isabelle
APPLICANT: Busseau, Isabelle
APPLICANT: Busseau, Isabelle
APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: DATIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: NEW YORK
CITY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 aagaacggaggcctatggaggcccatgaggggctgaacgtcacagcaacaggcgcagg 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  975 GTTTCACCAAGGGATACGCCCCTGTTGGGTACGCCGAATGCTGCCATGGGTCCGCTGG 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 tctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctggaggattat 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/185,432

FILING DATE: 21-JAN-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-006

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPHONE: (214) PENNIE
REFERENCE/DOCKET NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                              TELEPHONE: (212) 790-9090
TELERAX: (212) 869-8864/9741
TELEX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 gcctgcccacgccctttattttgc 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           915 GTTGGCGCACGTGGGTGAGATTGC 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/08185432 Patent No. 5750652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                 345..2558
                                                                                                                                                                                                                                       TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
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; LOCATION:
US-08-185-432-3
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US-08-185-432-23
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2797 GTTTCACCAAGGGATACGGCGCCTGTTGGGTACGCCGAATGCTGCGCATGGGTCCGCTGG 2856
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Patent No. 5972643

GENERAL INFORMATION:
APPLICANT: Lobanenkov, Victor V.
APPLICANT: Neiman, Paul E.
APPLICANT: Rienova, Elena M.
APPLICANT: Filippova, Galina W.
APPLICANT: Filippova, Galina N.
APPLICANT: Collins, Steven J.
TITLE OF INVENTION: CTCF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,844
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                 Query Match 9.5%; Score 27.2; DB 1; Best Local Similarity 49.3%; Pred. No. 11; Matches 71; Conservative 0; Mismatches 73;
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FILING DATE: ...
FILING DATE: ...
APPLICATION DATA:
APPLICATION NUMBER: 08/261,680
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PATHELE, Steven W
REGISTRATION NUMBER: 14538
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2857 GTTGGCGCACGTGGGTGAGATTGC 2880
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nucleic acid
EDNESS: double
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                              ; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-185-432-23
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USA
    TYPE: nucleic STRANDEDNESS:
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ORIGINAL SOURCE:

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UMEDIATE SOURCE:
CLONE: human CTCF CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 292..2475
FEATURE:
NAME/KEY: exon
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OTHER INFORMATION: /label= exon3
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US-08-475-844-8
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; 0 0; Gaps Query Match 9.5%; Score 27.2; DB 2; Length 3810; Best Local Similarity 64.1%; Pred. No. 11; Matches 41; Conservative 0; Mismatches 23; Indels 0;

QQ

105 gaac 108 ò

Search completed: September 28, 2002, 07:56:00 Job time: 11245 sec

BI854643 603381569 BI876051 f167c03.y BJ039504 BJ039504

BE012485 121949 MA

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butheria; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 747)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LiAM11422 row: a column: 23
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BG777404 602664685
AKO06155 Mus muscu
B1449976 dac76f09.
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BI757180 603028871
BJ035232 BJ035232
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                                   AV704087 AV704087
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Location/Qualifiers
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AI310713
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AL654963
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BB654057
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DEFINITION
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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BI827322
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KEYWORDS
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SOURCE
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B1541703 455541 MA
BE913718 601669072
BG964218 601828996
BG295496 602328286
B1794616 1C92e02. Y
B1185580 UNL.-P-FN-
AW211366 uo80b07. Y
B1831943 603076873
AW326482 19106 MAR
                                                             ; Search time 4881.77 Seconds (without alignments) 787.959 Million cell updates/sec
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                                                                                                                     1 atgcagagtctacagcctga......tgaaccctgcggaaggctga 285
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       4.5
Compugen Ltd
                                                                                                                                                                   13736207 segs, 6748477542 residues
                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                              September 28, 2002, 06:22:48
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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BI194616
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                                           OM nucleic - nucleic search, using sw model
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length: 2000000000
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Minimum DB seq Maximum DB seq

Database

Perfect score:

Run on:

Scoring table: Sequence:

Searched:

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BII03329 602888838 BM488747 pgm2n pk0 BI412175 602955377 BF916224 CM2-UT011 BI739710 603361983

Score

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Result

280 227.6 227.6 225.8 225.8 2246.8 2246.8 2246.8 234.2 234.4 223.4 223.4 223.4 195.4 1195.4 1195.4 1196.4 1196.4

cloning). Average insert size 1.3 kb, insert size range

BB644566 BB644566 BG895490 358967 MA AA061624 mj90h11.r

AZ693917 AST-2HLB2

BI831750 603079016

AW210205 u152b03.y AI133696 HA2320 Hu

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Ouery Match
Best Local Similarity
Matches 278; Conserv
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COMMENT
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BIO45863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
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0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NHWGC Library." 1 others
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li, Wass, Gruber.C., Jessee,J. and Polayes,D.

Full.length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                     61 aggattataagaacggagggcctatggaggcccatgaggggggctgaacgtcacagcaaca 120
                                                                                                                                                                                                                                                                                        121 ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
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BP 191 91006 EVRX cedex - France
Email: segreféquenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                    Length 747;
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3.1e-76;
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                                                                                                                                  98.2%; Score 280; DB
100.0%; Pred. No. 3.1
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Genoscope
                                                                                                                                                                    Matches 280; Conservative
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Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 480)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W.Jr., Zago, M.A., Bordin, S., Costa, F.F.

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-FN0209-300101-004-h10&t3-2001-01-30&t4=1)
Seq primer: puc lB forward
High quality sequence stop: 480.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                        477 AGGATTATAAGAACGGAGGGCCTATGGAGGCCCATGAGGGGGCTGAACGTCACAGCAACA 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtg
                                                                                                                                                                                                                                                                                                                                                    ggcgcagggcctgcccacgccctttattttgcctgctacgaaaaagttaaaaaagacattg
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        Length 888;
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                              Indels
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Score 277.6; DB 9
Pred. No. 1.8e-75;
1; Mismatches 1.
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/db_xref="taxon:9606"
/clone_lib="FN0209"
/dev_stage="Adult"
     97.4%;
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                                                              Conservative
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AUTHORS
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JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 573)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Cassas, E., Waray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 30-AUG-2001
application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                      1;
                                                                                                                                     Length 480;
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455541 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
BI541703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4390
Fax: 402 762 4390
                                                                                                                                   Score 265.8; DB 10;
Pred. No. 7.2e-72;
0; Mismatches 2;
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Location/Qualifiers
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                                                                 146 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI541703.1 GI:15382815
                                                                                                                                  93.3%;
98.9%;
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                                                                                                                                                   Best_Local Similarity 98.9
Matches 278; Conservative
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S NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robers Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lini.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
              /tissue_type="pooled"
/lab_host="HH10B"
/note="Vector: pcMV SPORT6; Site_1: Xba1; Site_2: Xho1;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 GGCGCAGGGCCTGCCCACGCCCTCTATTTTGCCTGCTATGAAAAGTTAAAAAAAGACATTG
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                                                                                                                                                                                                                                   Length 573;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                   Score 257.4; DB 10;
Pred. No. 3.1e-69;
                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                 0; Mismatches
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/db_xref="taxon:10090"
/clone_lib="MARC 1BOV"
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94.3%;
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BE913718
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Mus musculus
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                                                                          Similarity
                                                        Query Match
Best Local Simi
Matches 260;
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ORIGIN
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TITLE
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BG295496
LOCUS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.; I (bases 1 to 645)

National institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Colome distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC Column: 24

High quality sequence start: 2

High quality sequence start: 2

Location (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/brain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4983815"
/clone="Ib="NCI_CGAP_CO24"
/lab_host="DHIOB (TI phage-resistant)"
/lab_host="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
Primer: Oligo dT
                Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" _{\rm I} 172 g _{\rm I} 110 t
                                                                                                                                                                                                                                                                                    61 aggattataagaacggaggcctatggaggcccatgaggggctgaacgtcacagcaaca 120
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                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      ő
                                                                                                                                  DB 10; Length 598;
                                                                                                                                                                        22; Indels
Site_2: NotI; Cloned unidirectionally.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.6%; Score 246.8; DB 1
92.2%; Pred. No. 6.2e-66;
iive 0; Mismatches 22
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BG295496
602392826FI NIH_MGC_94 Mus musculus cDNA clone IMAGE:4504638 5',
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ub_Arts__caxu...vv.v.
/clone="InAGC_1454638"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH108 (phage-resistant)"
/lab_host="DH108 (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
/Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
/Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                               173 ATGCAGAGCCTACAGCCTGACCCAGCCGCCCCGTTCGGAACGTGTTGGAGGCTCTCTGG 232
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Score 246.8; DB 10
Pred. No. 6.3e-66;
0; Mismatches 22,
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/db_xref="taxon:10090"
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  86.6%;
92.2%;
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BG295496
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86.6%; Score 246.8; DB 10; Length 1131;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillar, L., Marra, M., Pape, D., Wylle, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Taagareishvili, R., Williams, T., Endocrine Pancreas Consortium
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 560)
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Cohter_ESTS: 1629-02.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Endocrine Pancreas Consortium
Bravard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 430.

Location/Qualifiers
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                                                                         aggattataagaacggagggcctatggaggcccatgaggggggctgaacgtcacagcaaca 120
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ches 22;
92.2%; Pred. No.
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BI794616
BI794616.1 GI:15822341
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                       260; Conservative
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/note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I; Five libraries representing E10.5/12.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SupersCript Plasmid Library kit (Life Technologies). CDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; O.5 microgram single-stranded mixed library plasmid DNA was mixed and bybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
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1 (bases 1 to 574)

5 Gaetano, A.R., Johnson, R.K. and Pomp, D.

Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles

L upublished (2001)

Contact: Pomp, D.

University of Nebraska, Lincoln

Lincoln, NE 6883.0908, USA

Tel: 402 472 6416

Fax: 402 472 6362
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Pred. No. 1.9e-65;
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Alab_host=""DH108" (Life Technologies)"

Anote=""Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1: Site_2: Eco RI; The UWL-P-FN library is a normalized library representing porcine ovarian follicles, ranging between 2.0 to 10.0 mm in diameter, collected during 7 days of the follicular phase of the pig estrous cycle. This library was derived from the library UWL-P-F2. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW21136b 11 Dp mRNA linear EST 03-DEC-1999 UNBOBDOT.yl NCI_CGAP_Mam3 Mus musculus CDNA clone IMAGE:2648821 5' similar to WP:W02B12.9 CE03769 MITOCHONDRIAL RNA SPLICING MSR4 LIKE PROTIELN ;, mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index University (CGAP), Unpublished (1997)
                                                   /strain="University of Nebraska, Lincoln Swine Selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Brail: gapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 574;
                                                                                                                                                                                                                                                                                                                                                                                              2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 244.6; DB 10; Length
Pred. No. 2.9e-65;
0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 ANAACATTACTTCATGATGCAGCCATGAATCCAGCAGAAG 413
                                                                                                       /clone_"UNL-P-FN-cy-f-02-0-UNL"
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                       by Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                              ų
                                                                                                                                                                                                                                                                                                                                                                                            104
                                 /organism="Sus scrofa'
                                                                                      /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                          TAG_SEQ=None found"
171 c 165 g
Location/Qualifiers
                                                                                                                                          /dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW211366.1 GI:6517318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.8%;
94.3%;
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Matches 264; Conservative
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                  source
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LOCUS
DEFINITION
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/organism="Mus musculus"
/strain="129 - C57/B6 - FVBN"
/db_raref="taxon:10090"
/clone="lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/tissue_type="tumor, gross tissue"
/dab_nost="DH10B"
/lab_nost="DH10B"
/note="Organ: mammary: Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999).
98 t
                     DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI831943 701 bp mRNA linear EST 04-0CT-2001 603076873F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5168539 5', mRNA sequence.
BI831943. GI:15943493
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 aggattataagaacggaggcctatggaggcccatgaggggggctgaacgtcacagcaaca 120
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausherg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement. Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 5.6e-62;
0; Mismatches 20
                                                                                                   www-bio.llnī.gov/bbrp/image/image.html
                                                                                                                                                                            Seq primer: -40RP from Gibco
High quality sequence stop: 427
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 GCGACATTACTTCATGATGCAGCCCT 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.1%;
92.5%;
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Best Local Similarity 92.5
Matches 246; Conservative
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Contact: Smith TPL
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SOURCE
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1 (bases 1 to 336)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: They Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.a column: 20
High quality sequence start: 29
High quality sequence stop: 699.
Location/Qualifiers
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0
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Pred. No. 5.9e-59;
0; Mismatches 1; Indels
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19106 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
AW326482
AW326482. GI:6762403
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/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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MEDLINE
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Single pass sequencing. Bases called and trimmed with phred v0.890904.e. vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
FOR PRIMERS
FOR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BII03329 817 bp mRNA linear EST 26-JUN-2001 6028888838F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5043992
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 817)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgt 240
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Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cORA Library Preparation: Life Technologies, Inc.
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fex: 402 762 4390
                                                                                                    Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref-"taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 8 row: F column: 16
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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BI103329
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USA

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AUTHORS
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                                                                                                                         FEATURES
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                                                                                                                                                                                                                                                                                    /strain="FVBN" "Colore" Independent of the colore independent of the colore independent of the colore independent of the colore independent of the color of the c
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
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Cogburni.L.A. and Monsonego-Ornan,E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1120 row: 1 column: 09
High quality sequence stop: 777.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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University of Delaware
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/dev_stage="Breast.leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(ld,7d,14d post-hatch)"
/lab.host="E. coli EMDH108"
/note="vector: pcw/SpORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
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602965377F1 NCI_CGAP_Lu33 Mus musculus CDNA clone IMAGE:5120755 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                            /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
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NIH-MGC http://mgc.nci.nih.gov/.
NAH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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                                                                                                                                                                    Ottawa Res. Centre
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/clone_libe"Normalized Chicken Breast Muscle, Le
and Epiphyseal Growth Plate cDNA library (pgm2n)
/sex="Male and Female"
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Pred. No. 5.7e-50;
0; Mismatches 54; Indels
Fax: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
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/strain="Commercial broiler
strains 90 & 21"
/db_xref="taxon:9031"
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80.78;
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Best Local Similarity 80.7'
Matches 226; Conservative
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

us-09-870-113-9.rst

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NOI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11294 row: j column: 20
High quality sequence start: 7
High quality sequence start: 7
High quality sequence stop: 809.
Location/Qualifiers
1. 855
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Bonaldo, Ph.D.
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AC09368 Rattus no
AF2161699 Mus muscu
AF216674 Homo sapi
AX306258 Sequence
BC015013 Homo sapi
AC051642 Homo sapi
AC051642 Homo sapi
AC051642 Homo sapi
AC05172 Mus muscu
265521 Caenorhabdi
AF217402 Drosophil
AF217402 Drosophil
AF2097 Onchocerca
AC06797 Sequence
AP00317 Oryza sat
AC06797 Sequence
AP10846 Homo sapi
AF108461 Homo sapi
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AF1185 Praesityum
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AI1889 Traesityum
AC037522 Homo sapi
AC07552 Homo sapi
AC07552 Homo sapi
AC07552 Homo sapi
                                                                          A3303078 Homo sapi
AL353119 Human DNA
AC09531 Rattus no
AF286621 Mus muscu
AF223466 Homo sapi
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    X061229 Sequence
F327402 Homo sapi
Aj303077 Homo sapi
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1322)
Lal,P., Yang,J., Yue,H., Hillman,J.L., Tang,Y.T., Bandman,O.,
Burford,N., Baughn,M.R., Azimzai,Y., Lu,D.A., Au-Young,J. and
Patterson,C.
                                              AX071440 Sequence
AF327403 Homo sapi
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Patent: WO 0078933-A 76 28-DEC-2000;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Sequence 76 from Patent WO0078953.
AX061229 GI:12406365
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LQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLS
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Li,F., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R.
Larsson,C. and Suomalainen,A.
Direct Submission
Submitted (08-DEC-2000) Human Molecular Genetics, National Public Health Institute, Mennerheimintie 166, Helsinki 00300, Finland
Location/Qualifiers
1. 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to mitochondrial RNA splicing protein 3/4;
alternatively spliced"
/codon_start=1
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Homo sapiens putative mitochondrial solute carrier splice variant
mRNA, complete cds, alternatively spliced, nuclear gene for
AP30740?
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(Dases I to 1448)

Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R., Larsson,C. and Suomalainen,A.

Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
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                                                                                                                                                                                                                                 70.7%; Score 280; DB 9; I
ilarity 100.0%; Pred. No. 1.3e-81;
Conservative 0; Mismatches 0;
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(Rel. 67, Last updated, Version 2)
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/organism="Homo sapiens"
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nes 280; Conserv
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ARNA linear PRI 02-MAY-2001 HOMO sapiens putative mitochondrial solute carrier splice variant mRNA, complete cds, alternatively spliced, nuclear gene for mitochondrial product.
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LTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLL
NTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAMSVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1889)
Li,F., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R.
Larsson,C. and Suomalainen,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to mitochondrial RNA splicing protein 3/4;
alternatively spliced"
/codon_start=1
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1 (bases 1 to 1889)

Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen,R., Larsson,C. and Suomalainen,A.

Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (08-DEC-2000) Human Molecular Genetics, National Public
Health Institute, Mennerheimintie 166, Helsinki 00300, Finland
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                                                                                                                                                                                                                        ggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattgagtgatg
                                     9 GTCTACAGCCTGACCCAGCTGCCCGCTATCGCAATGTGTTGGAGGCCCTCTGGAGGATTA
                                                                                     taagaacggagggcctatggaggcccatgaggggggctgaacgtcacagcaacaggcgcag
                                                                                                                                                                                        129 GGCCTGCCCACGCCCTTTATTTTGCCTGCTACGAAAAGTTAAAAAAAGACATTGAGTGATG
                     gtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctggaggatta
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FEBS Lett. 494 (1-2), 79-84 (2001)
21195335
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/db_xref="GI:13926050"
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/db_xref="taxon:9606"
/chromosome="10"
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                              /product="mitochondrial RNA splicing protein 3/4"
//function="putative mitochondrial solute carrier"
//protein_id="CAC27996.1"
//translation="MELEGRAGGVAGGPAAGFGRSPGESALLDGWLORGVGRGAGGGE
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PDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKFILSDVI
                                                                                                                                HPGGNSHIANGAAGCVATLIHDAAMNPAEVVKORWOMYNSPYHRYTDCVRAVWONEGAG
AFYRSYTTQLIMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTP
LDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTA
                                                                                                                                                                                                                                                                                                            0;
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Milliams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Raihard, C., Raddazzo, F., Kennedy, G.C., Pot, D., Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M., Haman genes and gene expression products

Patent: WO 0102568-A 1912 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
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100.0%; Pred. No. 1.3e-81;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.1e-79;
Live 0; Mismatches 0;
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/db_xref="taxon:9606"
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4 c 120 g
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                 /gene="HMRS3/4"
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Best Local Similarity 100.
Matches 273; Conservative
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TMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNT
QESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-DEC-2000) to the EMBL/GenBank/DDBJ databases.
Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
                                            ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
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Larsson C., Suomalainen A.;
"Characterization of a novel human putative mitochondrial transporter
homologous to the yeast mitochondrial RNA splicing proteins 3 and 4";
FEBS Lett. 494:79-84(2001).
                                                                                              aggattataagaacggagggcctatggaggcccatgagggggctgaacgtcacagcaaca 120
                                                                                                                                                        mRNA for mitochondrial RNA splicing protein 3/4 (HMRS3/4
                        Gaps
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/function="putative mitochondrial solute carrier"
/protein_id="CAC27997.1"
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                       Indels
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            2.5e-63;
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                       Mismatches
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1032. .1565
            Pred. No.
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100.08; FIL
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/gene="HMRS3/4"
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(Rel. 67, Last upd
                       Matches 225; Conservative
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            Best Local Similarity
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26-APR-2001
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Nikali K.;
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Ramsay. H.

Direct Submission

Direct Submission

Direct Submission

Submitted (25-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonereques/@sanger.ac.uk

On Sep 26, 2001 this sequence version replaced gi:14280413.

During sequence assembly data is compared from overlapping clone
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality) =
30); an attempt was made to resolve all sequencing problems, such
one plasmid subclone or more than one M13 subclone: and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; SW.,
SWISSPROT; Tr., TREMBL; WP., WORMPEP, information on the WORMPEP

database can be found a we.
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RP11-85A1 is from the library RPC1-11.1 constructed by the group of
Ppieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL353719 123160 bp DNA linear PRI 25-SEP-200:
Human DNA sequence from clone RP11-85A1 on chromosome 10, complete
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WECTOR: This sequence is not the entire insert of clone inpopyrary: This sequence is not the entire insert of clone RPI1-85A1 It may be storten because we sequence overlapping sections only once, except for a short overlap. This sequence. The true left end of clone RPI1-85A1 is at 1 in this sequence. The true left end of clone RPI1-83811 is at 12361 in this sequence. The true right end of clone RPI1-129J12 is at 51589 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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                                                                                                                                                                                                                                                                                                                           aggattataagaacggaggcctatggaggcccatgagggggggctgaacgtcacagcaaca 120
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Catarrhini; Hominidae; Homo
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                                                                     Indels
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                                                              Mismatches
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Mammalia; Eutheria; Primates;
56.00,
100.0%; Pie
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AL353719.10 GI:15787725
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                                 Similarity 100.
25; Conservative
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Matches 225;
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TITLE
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Natures:

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Natures:

National Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,

Benton, J., Buimage, K., Blankenburg, K., Bonnin, D., Bouck, J.,

Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,

Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,

Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R.,

Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,

Davy-Carroll, L., Dederich, D.B., Delaney, K.R., Delager, H.,

Davy-Carroll, L., Dederich, D.B., Delaney, K.R., Draper, H.,

Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,

Elhaj, C., Esoctto, M., Falls, T., Ferraguch, D., Garcia, A., Garner, T.,

Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hawes, A.,

Hennandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,

Hollins, B., Homsi, F., Howard, S., Huber, J., Hilyk, S., Hume, J.,

Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,

Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,

Kovar, C., Kratovic, J., Kureshih, A., Landry, N., Leal, B., Lewis, L.C.,

Lewis, L., Li, J., Li, Z., Lichtarge, O., Liu, J., Liu, M.,

Lewis, L., Li, J., Liu, J., Liu, J., Liu, M., Liu, J., Liu, M.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone="RP11-85A1"
/clone=lib="RPC1-11.1"
complement(7066. .7118)
/note="Single clone region. Sequence from reads from a
short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."
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100.0%; Pred. No. 5.1e-63;
ive 0; Mismatches 0;
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                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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HTG: HTGS_PHASE1; HTGS_DRAFT.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 56.8
Best Local Similarity 100.
Matches 225; Conservative
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Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., Martin, P., Meador, M., Merzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Nayen, N., Nickerson, E., Nwokenwo, S., Nayen, N., Nickerson, E., Nwokenwo, S., Oguh, M., Okwuon, G., Oragunye, N., Oyiedo, R., Pace, A., Payton, B., Perry, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quilse, M., Rolse, M., Rolse, M., Savery, G., Scherer, S., Scott, G., Shen, H., Shosshtari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamarisa, R., Tansey, J., Taylor, C., Taylor, P., Tamarisa, R., Tansey, J., Taylor, C., Taylor, T., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Naron, E., Man, S., Man, S., Man, S., Walls, R., Wang, S., Wall, Wall, S., Wall, S
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NOTE: This is a "working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15627972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 200164 bases at least Q40
Consensus quality: 205303 bases at least Q30
Consensus quality: 209366 bases at least Q30
Estimated insert size: 209880; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 3.9x in Q20 bases; sum-of-contigs estimation
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of 6947 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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Direct Submission
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ROD 27-OCT-2001
                                                                                                                                                                                                   1 (bases 1 to 4112) Li,Q.-Z., Ruan,Q.-G., Eckenrode,S., Shi,J.-D., Cruz,P., Wang,C.-Y. and She,J.-X.
                                                                                                                                                                                                                                                                                                    Submitted (20-JUL-2000) Pathology, University of Florida, 1600 SW Archer Road, Rm. D6-15, Gainesville, FL 32610, USA Location/Qualifiers
1. .4112
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                AF288621 4112 bp mRNA linear ROD 27-(
Mus musculus mitochondrial solute carrier-like protein mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.2%; Score 139.2; DB 10; Length 4112; 68.6%; Pred. No. 9.4e-35; Live 0; Mismatches 88; Indels 0;
                                                                                                                                                                                                                                A new gene which is highly expressed in NOD mice spleen Unpublished
                                                                                                                                                                                                                                                                       Li,Q.-Z., Shi,J.-D., Cruz,P., Echenrode,S., Ruan,Q.-G. Wang,C.-Y.
gcaacattacttcatgatgcagccatgaaccctgcggaag 280
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/db_xref="taxon:10090"
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                   nr.223466 1429 bp mRNA linear PRI 17-APR-2000
Homo sapiens HT015 protein (HT015) mRNA, complete cds.
AF223466
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YEFLOEOVNPHRTYNPQSHIISGGLAGALAAAATTPLDVCKTLLNTOENVALSLANIS
GRLSGMANAFRTVYQLNGLPATSKASRRVSSTRCPPPPFLGLSMSSSSTFSPSASWKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MELRSGSVGSQAVARRMDGDSRDGGGKDATGSEDYENLPTSAS
VSTHMTAGAMAGILEHSVMYPVDSVKTRMOSLSPDPKAQYTSIYGALKKIMRTEGFWR
PLRGVNVMIMGAGPAHAMYFACYENMKRTLNDVFHHQGNSHLANGIAGSMATLLHDAV
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                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1429)
                                                                                                                                                                                                                                                                   Song, H., Gao,G., Peng, Y., Ren,S., Chen,Z. and Han,Z.
Direct Submission
Submitted (12-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
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Pred. No. 4.1e-31;
0; Mismatches 95; Indels
                                                                                                                                                                                                   Song, H., Gao, G., Peng, Y., Ren, S., Chen, Z. and Han, Z. A novel gene expressed in human hypothalamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 gcaacattacttcatgatgcagccatgaaccctgcggaag 280
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/tissue_type="hypothalamus"
1. .1429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="HT015 protein"
/protein_id="AAF64141.1"
/db_xref="G1:7578783"
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Best Local Similarity 66.1%;
Matches 185; Conservative 0
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RESULT 10
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Ruzny, D.M., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Alabronks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Blanksy, D.M., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Blanksy, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burton, T.F., Button, P., Burkett, C., Burterli, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavaz, D., Chen, G., Chen, R., Cavaros, S.R., Darid, R., Davila, M.L., Davis, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.D., Cox, C., Davy, Carroll, L., Dederich, D.A., Delaney, R.R., Delgado, O., Dugan-Rocha, S., Durbin, K.J., Earnbart, C., Edapar, D., Edapar, H., Bugan-Rocha, S., Durbin, K.J., Earnbart, C., Edapar, D., Edapar, M., Fort, J. Foster, P., Frantz, P., Cableil, A., Gao, J., Garcia, A., Garre, T., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garre, T., Harris, C., Harris, C., Harris, K., Harris, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, C., Katovic, J., Harris, K., H
ACUMY 358 11near HTG 20-DEC-2001 Rattus norvegicus clone CH230-84611, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces.
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On Dec 20, 2001 this sequence version replaced gi:16901901.
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as Trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 146548 bases at least Q20 Estimated insert size: 120308; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation
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7 agtetacagectgacccag-ctgecegetategeaatgtgttgga-ggeeetetggagga 64 Length 163205 5 Indels bp in length in length in length bp in length bp in length in length bp in length in length length in length length in length in length in length in length in length in length bp in length in length in length in length in length length Length length ength length ength ength length length length ength Length length ength. length ength ength ength Length ength Length ength ength unknown length ength ength Length ŗ Ţ DB 2; Score 125.2; DB 2 Pred. No. 7.9e-30; unknown of 1137 1481 0; Mismatches 1479 1050 2010 1137 1988 1916 1080 1699 unknown 1354 of 1649 unknown 2423 unknown of 1846 2088 unknown 1140 unknown 1960 unknown 1006 unknown of 1938 unknown of 2037 1574 unknown 1651 unknown unknown of 1634 unknown of οĘ contig gap of contig contig gap of contig gap of contig gap of contig gap of gap of contig contig contig gap of contig contig gap of contig gap of contig gap of contig gap of gap of contig gap of contig contig gap of gap of 31.6%; 87.4%; 99814: 142626: 99914: 100964: 16312: 08922 13156 28790 10868 35838 37589 137689 39043 140877 04311 140777 Query Match
Best Local Similarity 87.4'
Matches 194; Conservative 99815 99915 100965 101065 103175 104312 106935 106935 110869 110869 35839 137590 139144 140878 114297 114397 116313 116413 117493 117593 1119553 1120659 120759 121896 121896 121896 1213373 134072 113057 113157 126992 35939 25411 30928 32502 32602 26892 30828 39044 25311

5

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 1 AF361699

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE

TITLE JOURNAL

FEATURES

CDS

AUTHORS JOURNAL REFERENCE

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AC108878 191702 bp DNA linear HTG 06-FEB-2002
Mus musculus clone RP23-256H24 strain C57BL6/3, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://wchanning.bwh.harvard.edu:9088/hpcgg/jsp/hpcgg/Sequence/mous
e.html
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toases 1 to 191702)
Grills,G. Li,L., Montgomery,K.T., Brown,W.A., Chiu,D., Decker,J., Fusina,M., Haider,A., Keller,A., Perera,A., Shim,C., Thomas,E., High Throughput Mouse Sequencing Rucherlapati,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-FEB-2002) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA 02139, USA on Feb 6, 2002 this sequence version replaced gi:18464039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: AKY
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 18721 at least Q20
*Consensus quality: 183181 at least Q40
*Consensus quality: 183181 at least Q40
*Estimated insert size: agarose-FP - N/A
**Estimated insert size: J1382 - sum-of-contigs
Quality coverage: agarose-FP - N/A
Quality coverage: 5.6 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grills,G., Li,L., Montgomery,K.T., Brown,W.A., Chiu,D., Decker, Evsina,W., Haider,A., Keller,A., Perera,A., Shim,C., Thomas,E., Zencheck,W., Xi,C., Juels,P. and Kucherlapati,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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vsthwtagamagilehsimypvdsvktrmqsinpdpkarytsiygalkrimhtegfwr
Plrginvmmmgagpahamyfracyenwkrtlndvfshqgnshlangilkafvwsweall
                                                                                                                     5869 bp mRNA linear ROD 07-NOV-2001 nuclear gene for mitochondrial product. AF361699
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
1 (bases 1 to 5869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A novel mouse mitochondrial carrier protein gene is up-regulated from young to adult NOD mice Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (15-MAR-2001) Department of Pathology, Immunology and Laboratory Sciences, University of Florida, 1600 SW Archer Road, Room D6-15, Gainesville, FL 32610, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,Q., Eckenrode,S., Wang,C., Ruan,Q., Shi,J., McIndoe,R.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 5869)
51,0., Eckenrode,S., Wang,C., Ruan,Q., Shi,J., McIndoe,R.A. and
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/product="micochondrial carrier-like protein"
/protein_id="AAL27990.1"
/db_xref="G1:1675528"
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0; Mismatches 72; Indels
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1427 c 1390 g 16
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/db_xref="taxon:10090"
/chromosome="14"
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68.0%;
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/note="MCLP"
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Query Match

BASE COUNT ORIGIN

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1 (bases 1 to 108765)
Schilhabel,M.B., Baumgart,C., Blechschmidt,K., Dette,M., Jahn,N., Lehmann,R., Menzel,U., Polley,A., Reichwald,K., Schudy,A., Siadiquii,R., Taudien,S., Wen,G., Schlegelberger,B., Siebert,R., Chromosome 8 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 106283 ATGCAGAGTTTGAATCCAGATCCCAAAGCCCGGTATACAAGCATCTATGGCGCCCTCAAG 106342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 106343 AGGATCATGCACACTGAAGGCTTCTGGAGGCCCCTGCGGGGCCTGAACGTGATGATG 106402
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Polley,A., Wen,G., Baumgart,C., Dette,M., Jahn,N., Schilhabel,M.,
Menzel,U. and Rosenthal,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (15-DEC-1999) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
On Jun 2, 2001 this sequence version replaced gi:8151796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aggattataagaacggagggcctatggaggcccatgagggggctgaacgtcacagcaaca 120
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                                                                                                                      189584: contig of 1148 bp in length 189604: gap of unknown length 190648: contig of 1044 bp in length 190668 gap of unknown length 191702: contig of 1034 bp in length.
                    in length
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                                                                                     188416: contig of 2003 bp in length
188436: gap of unknown length
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Center code: IMB
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hes 72;
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                                                   contig of 2398
gap of unknown
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0; Mismatches
                  of 1367
                                    unknown
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/clone="RP23-256H24"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                    contig
                                    gap of
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                  .83975:
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182608:
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                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                         Sequencing vector: Mi3; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 87772 bases at least Q40
Consensus quality: 95159 bases at least Q30
Consensus quality: 100612 bases at least Q30
Quality coverage: 3,95 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently * consists of 16 contigs. The true order of the pieces * is not known and their order in this sequence record is
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Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
------ Project Information
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                                                              Center project name: H241
Center clone name: RP1-158P13
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Ishikawa,K., Asal,S., Takahashi,Y., Nagata,T. and Ishii,Y.
Ishikawa,K., or examining ischemic conditions
Patent: Wo 0188188-A 1009 22-NOV-2001;
School Juridical Person Nihon University (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 104.8; DB 6; Length 483;
Pred. No. 1.8e-23;
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/organism="Mus musculus"
/db_xref="taxon:10090"
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Search completed: September 28, 2002, 08:00:04 Job time: 14925 sec

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AAC74843 standard; cDNA; 1418 BP.
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/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:
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GenCore version 4.5
Copyright (c) 1993 - 2000. Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 2000000000
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396
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

:	ption	ORFX ORF398	polynucleoti	transport pr	uncoupling p	Novel human polynu	polynucleoti	secreted pro	immune/haema	immune/haema
	Description	Human	Human	Нишап	Human	Novel	Human	Human	Human	Human
Ş	1D	AAC74843	AA160661	AAF27733	AAC90457	AAF66156	AAI58875	AAS03906	AAK69779	AAK73320
í	8C :	21	22	22	23	22	22	22	22	22
S Query	rengru	1418	1294	1322	1336	401	1316	2502	27960	27960
Query	Match	71.0	70.7	70.7	70.7	68.8	68.7	56.8	56.8	56.8
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Human immune/haema Human polynucleoti Human mitochondria Human Oker ORE744 Human bone marrow Human gene express Human gene express	bone cDNA cDNA full- immun	Human full-length Human polymucleoti Human Okry ORFX ORFX 08 Human cDNA 5'-end Human cDNA 5'-end Human cDNA 5lone r Human secreted oro	Human secreted processors and secreted brosophila melanog Human immune/haema CDNA encoding nove Human ORFX ORF2246	Aspergizing oryzae Arabidopsis thalia Arabidopsis thalia Human immune/haema DNA encoding novel Blackcurrant pRIB7 Blackcurrant fruit	9000
AAK58672 AAK52172 AAF59920 AAC77189 AAH90057 AAZ13026	AAH89944 AAK92357 AAK93895 AAK94871 AAK80493	AAK94897 AAC91320 AAC77175 AAK91764 AAK93200	ABA83356 AAS62787 ABL08627 AAK80490 AAC76691	AAC39502 AAC39502 AAC39502 AAC39502 AAC39502 AAT68957 AAT68952	ABL08626 AAF26927 AAI71019 AAX60283
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339 1902 1305 1716 2562 300 710	1913 842 842 1814 2837 483	1890 3028 1468 622 622 1758	2037 2037 2137 8211 3842 6712	1371 1373 11800 1227 1311 5150	6326 355 1114 1363
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129.6 129.6 128 128 128 121	107.6 105 105 105 105	103.4 103.4 101.8 101 101 91.4	91.4 42.5 37.4 34.4	333.6 32.2 32.2 4.4 4.4	32.4 32 32 32
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ALIGNMENTS

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
w unticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic;
M pypotensive; dermatological; immunosuppressive; antiinflammatory;
W antiviral; antibacterial; antifungal; antithumatic; antithyroid;
antiannemic; gene therapy; cancer; proliferative disorder; hypertension;
m cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AlDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe compined immunodeficiency; malaria; autoimmune disorder; asthma;
m llergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound;
bone damage; cartilage damage; antiinflammatory disease; coaqulation;
thrombosis; contraceptive; ss. Human ORFX ORF398 polynucleotide sequence SEQ ID NO:795 08-FEB-2001 (first entry)

Homo sapiens.

WO200058473-A2.

05-0CT-2000

31-MAR-2000; 2000WO-US08621.

(first entry)

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as central nervous system injuries
                                                                Human polynucleotide SEQ ID NO 4650.
                                                                                                                                                                                                                                                                                                                    26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                    WO200153312-A1
                                                                                                                                                                                  leukaemia; ss
                                                                                                                                                                                                                   Homo sapiens
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29-NOV-2000;
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                                22-OCT-2001
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AAI60661;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang
Zhao
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                                                                                                                                                                                                                                                                                                            AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX aguences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; antimunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antifungal; antitheumatic; antithyroid; and antibacterial; antiviral; antifungal; antitheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder nucleic acids can be used to express OREX proteins in gene therapy eccoust. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.0%; Score 281; DB 21; Length 1418; 100.0%; Pred. No. 2.9e-85; 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1418 BP; 353 A; 400 C; 368 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                5; Page 853-854; 5507pp; English.
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tive 0; N
            31-MAR-1999; 99US-0127607
02-APR-1999; 99US-0127636
05-APR-1999; 99US-0127728,
30-MAR-2000; 2000US-0540763,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 281; Conservative
                                                                                                                              Shimkets RA, Leach M;
                                                                                               (CURA-) CURAGEN CORP
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                                                                                                                                                               WPI; 2000-602362/57
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2000US-028723.7. 2000US-0552317. 2000US-059042. 2000US-0653450. 2000US-0653450. 2000US-0653450. 2000US-0653450. 2000US-0653450.

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Wang

Ren F,

Zhang J;

Yang Y,

Chen R, Ma Y, Xu C, Xue AJ, R, Drmanac RT;

Wehrman T, X Goodrich R,

Liu C, P Wang Z, W

OA,

2001-442253/47

Asundi V,

Qian XB,

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Query Match
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                                                                aggattataagaacggaggcctatggaggcccatgagggggctgaacgtcacagcaaca
                           aggattataagaacggagggcctatggaggcccatgaggggggctgaacgtcacagcaaca
                                                   ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg
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61
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AAI60661 standard; cDNA; 1294 BP

AAI60661/c ID AAI606 XX

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in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system of neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1134 AIGCAGAGTCTACAGCCTGACCCAGCTGCCCGCTATCGCAATGTGTTGGAGGCCCTCTGG 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.7%; Score 280; DB 22; 100.0%; Pred. No. 6.1e-85;
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Claim 1; SEQ ID NO 4650; 10078pp; English
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Matches 280;
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           aggattataagaacggaggcctatggaggcccatgaggggggctgaacgtcacagcaaca
                     agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtg
                                                ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg
                                                                                                                                                                                                                                                                     Human; uncoupling protein; immunosuppressive; antiarthritic;
                                                                                                                                  gcaacattacttcatgatgcagccatgaacctgcggaag
                                                                                                                                                                                                                                                  Human uncoupling protein cDNA #6.
                                                                                                                                                                                         AAC90457 standard; cDNA; 1336
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                                                                                                                                                                                                                                                Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder; immune disorder; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide with a human transport protein sequence is use for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular systems
1014 GGGGGAGGGCCTGCCCACGCCCTTATTTGCCTGCTACGAAAAGTAAAAAAGACATTG
                                                                agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtg
                                                                           ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg
                                                                                                                                                                                                                                                                                                                                                                                                                               Bandman O,
Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1322 BP; 328 A; 376 C; 351 G; 267 T; 0 other;
                                                                                                   Human transport protein TPPT-33 coding sequence
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                                                                                                                                                                     AAF27733 standard; cDNA; 1322
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99US-0148177.
99US-0149357.
99US-0162287.
                                                                                                                                                                                                                                                                                                                                            2000WO-US16668
                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-041424/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAB60113
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                                                                                                                                                                                                                                                                                                        WO200078953-A2.
                                                                                                                                                                                                                                                                                                                                                             17-JUN-1999;
10-AUG-1999;
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproductive,
                                                                                                                                                                                                                                                                                                                                            16-JUN-2000;
                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          28-OCT-1999;
                                                                                                                                                                                                          28-MAR-2001
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BP

(first entry)

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antirheumatic; antiproliferative; cardiant; vasotropic; erebroprotective, neuroprotective, antibacterial; opthalmological; gastrointestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding uncoupling proteins. The nucleotide sequences may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of eighteen isolated nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uncoupling proteins and nucleic acid sequences encoding them, usefu for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM, Ni J, Komatsoulis G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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99US-0149448.
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                                                                                                                                                       infertility; ss.
                                                                                                                                                                                                                                                                                                WO200061614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1999;
18-AUG-1999;
12-NOV-1999;
                                                                                                                                                                                                                               Homo sapiens
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Gaps 9

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Indels

DB 22; L 6.2e-85; hes 0;

Score 280; DB Pred. No. 6.2e 0; Mismatches

70.7%; Sc._ 100.0%; Pre 0; '

Matches 280; Conservative

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Similarity

Query Match Best Local S

Length 1322;

1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg

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AAI58875;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Innis MA, Garcia PD, Klinger J, Kassam A;
Kennedy GC, Pot D, Lamson G, Drmanac R;
Dickson M, Labat I, Leshkowitiz D;
LW, Strache-Crain B;
                                                                                 197 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg 256
                                                                                                                      180
                                                                                                                                agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtg 436
                          Gaps
                                             atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg
                                                                                                                      ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaaagacattg
                                                                                                                                                           agtgatgtaatccaccctggggggcaatagccatattgccaatggtgcggccgggtgtgtg
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Or
                                                                                                                                                                                                                                                                                                                                          cytostatic; gene therapy; colon cancer; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                          ;
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      Length 1336;
                          Indels
DB 21; Le
. 6.2e-85;
0;
                                                                                                                                                                                                       gcaacattacttcatgatgcagccatgaaccctgcggaag 280
                                                                                                                                                                                                                                                                                                                                                    breast cancer; lung cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                        Novel human polynucleotide, SEQ ID NO: 1912
                         Mismatches
      Score 280;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 818; 1046pp; English.
70.7%; Scor.
100.0%; Pre
0; 7
                                                                                                                                                                                                                                                                AAF66156 standard; cDNA; 401 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0142310.
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                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escobedo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Randazzo F,
, Drmanac S,
                          Conservative
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                 Similarity
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Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                         280;
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        Query Match
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                         Matches
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AAF66156
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                                                                                                                     ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                      or antisense oligonucleotides can be generated. The polynucleotides a their gene products are used as genetic or biochemical markers (e.g. blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to dysplasia and hyperplasia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         taatccaccctggggggaatagccatattgccaatggtgcgggccgggtgtgtggcaacat 247
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                                                                                                                                                                                                                                                                                                                                                                                                              gtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctggaggatta 68
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                                                                                                                                                                                                                                                                            Length 401;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                        Sequence 401 BP; 100 A; 104 C; 120 G; 76 T; 1 other;
                                                                                                                                                                                                                                                                          Score 273; DB 22;
Pred. No. 8.2e-83;
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                                                                                                                                                                                                                                                                                                                       Mismatches
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100.0%; Prer
0; N
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2000US-052317.
2000US-0598042.
2000US-062312.
200US-0653450.
2000US-0653191.
2000US-0633036.
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                                                                                                                                                                                                                                                                        Query Match 68.9°
Best Local Similarity 100.
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
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14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein; autoimmune disorder; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; bacterial infection; viral infection; ss; fungal infection; coular disorder; wound healing; tissue regeneration; epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
   Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtg 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 atgcatagtctacagtctgacccagctggccgctatcgcaatgtgttggaggtcctctgg 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggcctctgg 60
                                                                                                                      Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtg
                     Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 272; DB 22; Length 1316;
Pred. No. 3.3e-82;
0; Mismatches 5; Indels 0
 Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1316 BP; 335 A; 364 C; 337 G; 280 T; 0 other;
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                     Claim 1; SEQ ID NO 1078; 10078pp; English.
                                                                                                                                       such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein gene #25.
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Best Local Similarity 98.2%;
Matches 275; Conservative 0
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                                                                    WPI; 2001-442253/47,
 Liu C,
Wang Z,
                                     Zhou P,
                                                                                      P-PSDB; AAM39719
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                   Wang J, W
Zhao QA,
   rang YT,
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Sequences AASO3873-AASO3922 represent isolated nucleic acid molecules and PCR primers of the invention. acid of the invention. Secreted proteins and their related nucleic acids can be used in the diagnosis of or susceptibility to a pathological condition by determining the presence or susceptibility to a pathological condition by determining the presence or sheer a beence of a mutation in a nucleic acid or the presence or amount of expression of a secreted protein. The sequences are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The antibodies to the disorders and in diagnostic immunossays e.g. radioimmunoassays or enzyme disorders and in diagnostic immunossays e.g. radioimmunoassays or enzyme disorders and in diagnostic immunossays e.g. radioimmunoassays or enzyme diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardioxas necessably charteria, viruses and fungi and ocular disorders e.g. corneal infection. The peptides can also be used to aid wound healing and epithelial cell proliferation, to help prevent skin ageing due to sunburn, to maintain corgans before transplantation, to releproservative to alter storage capabilities.
                                                                                                                                                                                                                                                                                                                                      useful
                                                                                                                                                                                                                                                                                                                                    Forty one nucleic acid molecules encoding human secreted proteins, useful the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 aggattataagaacggagggcctatggaggcccatgagggggctgaacgtcacagcaaca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 agtgatgtaatccaccctggggggcaatagccatattgccaatggt 225
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                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 460-461; 518pp; English.
                                                                                                                                                                                                                                       CA;
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                                                                                                                  2000WO-US26324
                                                                                                                                                          99US-0155807
                                                                                                                                                                                                                                                                                               P-PSDB; AAU01950, AAU01989
                                                                                                                                                                                                                                       Komatsoulis G, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 56.8
Best Local Similarity 100.
Matches 225; Conservative
                                                                                                                                                                                                 (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                            2001-281684/29
                                     WO200123598-A1.
                                                                                                                  26-SEP-2000;
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Homo sapiens
                                                                             05-APR-2001
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ID AAK6
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 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24591
                                                                              17-JAN-2001; 2001WO-US01354
      (first entry)
                                                       WO200157182-A2
                                             Homo sapiens.
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Concers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent inwante/haematopoietic antigen genomic sequences from the present invention. AAK849421 to AAK84950 and AAM82169 represent sequences used in the exemplification of the present invention.
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                                       08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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Matches 225; Conservative
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amino acid sequences given in AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) cactivity, and can be used in gene therapy and vaccine production. (I) proteins and polynocleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting polynucleotides may be used to produce the secreted (I), by inserting the rotein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic artigen genomic sequences from the present invention. AAK84962 and AAM83269 represent invention. AAK84962 and AAM83269 represent invention.
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                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, immune, haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggcccttgg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3732
                                                                                                                                                                                                        Disclosure; SEQ ID NO 28132; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.8%; Score 225; DB 22; Length 27960; Best Local Similarity 100.0%; Pred. No. 1.7e-65; Matches 225; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK58672 standard; cDNA; 339 BP
(HUMA-) HUMAN GENOME SCI INC
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                                           Barash SC,
                                                                                 WPI; 2001-483426/52
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                                           Rosen CA,
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PR 29-SEP-2000; 2000US-0236370. PR 02-OCT-2000; 2000US-0237037. PR 02-OCT-2000; 2000US-0237037. PR 02-OCT-2000; 2000US-0237039. PR 13-OCT-2000; 2000US-0237039. PR 20-OCT-2000; 2000US-0241040. PR 20-OCT-2000; 2000US-0241040. PR 20-OCT-2000; 2000US-0241080. PR 20-OCT-2000; 2000US-024109. PR 20-OCT-2000; 2000US-0246477. PR 20-OCT-2000; 2000US-0246611. PR 20-OCT-2000; 2000US-0246611. PR 20-OCT-2000; 2000US-0246611. PR 20-OCT-2000; 2000US-0246611. PR 20-OCT-2000; 2000US-0246521. PR 20-OCT-2000; 2000US-0246521. PR 20-OCT-2000; 2000US-0246521. PR 20-OCT-2000; 2000US-0246521. PR 20-OCT-2000; 2000US-024921.	08-DEC-2000; 05-JAN-2001; 05-JAN-2001; (HUMA-) HUMA Rosen CA, B WPI; 2001-48 P-PSDB; AAM8
20001WO-US01354. 20000US-0180628. 20000US-0180628. 2000US-0180628. 2000US-0180628. 2000US-0180628. 2000US-0180644. 2000US-01908123. 2000US-01908123. 2000US-01908123. 2000US-01908123. 2000US-0118067. 2000US-0118068.	000000000000000000000000000000000000000
PR Y 17 - JAN - 2001, PR PR 31 - JAN - 2000, PR 24 - FEB - 2000, PR 26 - JUL - 2000, PR 27 - JUL - 2000, PR 22	21 - SEP 21 - SEP 25 - SEP 26 - SEP 27 - SEP 27 - SEP 29 - SEP 29 - SEP 29 - SEP 29 - SEP

Ruben SM;

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) and sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polyvuocleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/mamatopoietic antigen genomic sequences from the present invention. AAK84942 to AAK84950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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encoding human immune/hematopoietic antigen polypeptides, eventing, diagnosing and/or treating cancers and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 339;
                                                                  Claim 1; SEQ ID NO 3732; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 339 BP; 86 A; 84 C; 101 G; 64 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 174; DB 22;
Pred. No. 4.5e-49;
1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 717
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94.98;
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2000US-0560875
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Matches 188; Conservative
                useful for preventing, metastasis -
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 acids
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27-APR-2000;
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Best Local 3
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to erytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or eptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                       Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1458 aatgacgttttccaccaccaaggaaacagccacctagccaacgggatagctgggagtatg 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1278 atgcagagtttgagtccagatcccaaagcccagtacacaagtgtctacggagccctcaag 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1398 ggtgcagggccagcccatgccatgtattttgcctgctatgaaaacatgaaaaggacttta 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg
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                                                                                                                                                                     Wang 2W;
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0
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                                                                                                                                                   , Asundi V, Zhou P, Xu C,
Zhang J, Ren F, Chen R, Wa
, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1902 BP; 434 A; 532 C; 547 G; 389 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1518 gecaecetgetecacgatgeggtaatgaatecageagaag 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
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66.4%; Pred. No. 1.6e-33;
tive 0; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 gcaacattacttcatgatgcagccatgaacctgcggaag
                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2450-2452; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         were missing at the time of publication
                                                                                                                                                                                                                                                                                             useful in diagnosis and gene therapy
                                                                                                                                                                         Wang J, Zh
Wejhrman T,
                                                                                                                                                       Drmanac RT,
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            2000US-0620325.
2000US-0654936.
                                             2000US-0663561.
2000US-0693325.
                                                                                 2000US-0728422
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                                                                                                                                                     Liu C, |
Wang D,
Yang Y, |
                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                          P-PSDB; AAM79039
            19-JUL-2000;
01-SEP-2000;
                                             15-SEP-2000;
20-OCT-2000;
                                                                                 30-NOV-2000;
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                                                                                                                                                     Tang YT,
Zhao QA,
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                                                                                                                                                                                         Xue AJ,
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antidiabetic;

coaqulant; vasotropic;

immunostimulant; thrombolytic;

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0
                                                                                                                                                                                                                                                                                                                                                                                                   protein, hMSC-o (AAB60658), and cDNA encoding it (AAF5920). hMSC-o is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-o proteins and nucleic acids, and the detection of hMSC-o proteins and nucleic acids in a sample. The present sequence represents cDNA encoding hMSC-o.
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anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
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                                                                                                                                                                                                                                                                                                                          New human mitochondrion solute carrier protein and its nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel human mitochondrial solute carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggcgcaggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg
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              carrier protein; hMSC-o; hypothalamus;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.3%; Score 128; DB 22; Length 1305;
larity 66.1%; Pred No. 4.5e-33;
Conservative 0; Mismatches 95; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1305 BP; 292 A; 388 C; 363 G; 262 T; 0 other;
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                                                                                                                                                                                 17-MAR-2000; 2000CN-0114958
              solute
            Human mitochondrial solute preparation; detection; ss
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es 185; Conserv
                                                                                                                                                                                                                                                                           WPI; 2001-050544/
P-PSDB; AAB60658
                                                                                                                                                                                                                                              Gao X,
                                                          Homo sapiens
                                                                                        CN1269409-A
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                                                                                                                                                                                                                                              Zhang X,
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Matches
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                hypotensive, dermatological; immunosuppressive; artiinflammatory; antivital; antibacterial; antifundal; antithematus; antithematus; antithematus; antithematus; antithyood; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coagulation; to inhibit thrombosis; and as a contraceptive.
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66.1%; Pred. No. 5.2e-33;
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99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP
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                                                                                                                                                                                                                                                                   Homo sapiens.
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05-APR-1999;
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                      495
 aaaatcatgcggaccgaaggcttctggaggcccttgcgaggcgtcaacgtcatgatcatg 375
                                                                                                                                                                                                                                                                                       Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                 181 agtgatgtaatccaccctggggggaatagccatattgccaatggtgcggccgggtgtgtg
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                                                                                                                                      496 gecaccetgetecacgatgeggtaatgaatecageagaag 535
                                                                                                                  gcaacattacttcatgatgcagccatgaaccctgcggaag
                                                                                                                                                                                                                                                                    Human bone marrow cDNA, SEQ ID NO: 301.
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                                                                                                                                                                                               standard; cDNA; 2562 BP
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Zhao QA, Zhou P, Drmanac RT;
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2000us-0662191.
2000us-0693036.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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09-JUL-2000; 2
19-JUL-2000; 2
03-AUG-2000; 2
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19-OCT-2000; 3
30-NOV-2000; 2
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or more types of cancer. The polynucleotide and polypeptide can used as nutritional sources or supplements and in the screening chemical compounds as potential drugs.
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                                                                                                                                                                          Length 2562;
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                                                                                                        other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 gcaacattacttcatgatgcagccatgaacctgcggaag 280
                                                                                                                                                                          32.3%; Score 128; DB 22;
Similarity 66.1%; Pred. No. 6.4e-33;
35; Conservative 0; Mismatches 95;
                                                                                                      Sequence 2562 BP; 623 A; 660 C; 627 G; 652 T; 0
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98US-0072910.
98US-0075954.
98US-0080114.
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28-JAN-1998;
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Matches 185;
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                                                                                                                                                                                    Query Match
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Comprising the sequences given in AA212532 to AA21779. Also described is comprising the sequences given in AA212532 to AA21779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AA212532 to AA21779. The coll the 5248 polynucleotide sequence of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, be used for a variety of purpose, e.g. detection of expression levels, can be used for raising antibodies for experimental, diagnostic and therefore the polynucleotides can be used for raising antibodies for experimental, diagnostic and carrays for diagnostics (which may be used to determine function of an cencoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for contrible and an experimental cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
                              Claim 1; Page 774; 2479pp; English.
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Sequence 300 BP; 83 A; 76 C; 79 G; 62 T; 0 other;

ó Gaps 0; Query Match 30.6%; Score 121; DB 20; Length 300; Best Local Similarity 100.0%; Pred. No. 5.2e-31; Matches 121; Conservative 0; Mismatches 0; Indels (g ò g

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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/FOTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-185-432-3
US-08-185-432-23
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PCT-US95-08429-8
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US-08-537-361E-5
US-09-175-928-9
                                                                                                                                                                                                                                           383533 segs, 122816752 residues
                                                                                        September 28, 2002, 07:56:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                nucleic search, using sw model
                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_NA:*
                                                                                                                                            US-09-870-113-11
396
                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
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3810
5063
591
2379
3153
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Match 1
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                                                                                                                                                              Perfect score:
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Maximum DB s
                                                              OM nucleic
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                                                                                                                                                                                                                                           Searched:
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                                                                                          Run on:
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28 27 6.8 3508 4 US-08-462-467B-7 Sequence 7, Appli 30 27 6.8 3508 4 US-08-371-112A-1 Sequence 7, Appli 31 27 6.8 7824 5 PCT-0855-672-11 Sequence 11, Appli 27 6.8 7824 5 PCT-0855-60722-11 Sequence 11, Appli 27 6.8 7824 5 PCT-0855-60722-11 Sequence 11, Appli 31 26.8 6.8 1134 3 US-09-106-217-15 Sequence 11, Appli 32 26.8 6.8 1134 3 US-09-106-217-1 Sequence 11, Appli 35 26.8 6.8 1255 1 US-08-518-78-78-8 Sequence 38, Appli 37 26.8 6.8 1255 1 US-08-518-78-8 Sequence 38, Appli 38 26.8 6.8 1255 1 US-08-294-522B-38 Sequence 38, Appli 39 26.8 6.8 1596 3 US-09-210-681-38 Sequence 38, Appli 39 26.8 6.8 1596 3 US-09-210-681-38 Sequence 38, Appli 44 26.8 6.8 246240 2 US-08-724-394A-21 Sequence 20, Appli 44 26.8 6.8 246240 2 US-08-724-394A-21 Sequence 21, Appli 44 26.8 6.8 246240 2 US-08-724-394A-22 Sequence 21, Appli 45 26.8 6.8 246240 2 US-08-724-394A-22 Sequence 22, Appli 45 26.8 6.8 246240 2 US-08-724-394A-22 Sequence 22, Appli 45 26.8 6.8 246240 2 US-08-724-394A-22 Sequence 22, Appli 45 26.8 6.8 246240 2 US-08-724-394A-22 Sequence 22, Appli 45 26.8 6.8 246240 2 US-08-724-394A-22 Sequence 22, Appli 45 26.8 6.8 246240 2 US-08-724-394A-22 Sequence 22, Appli 45 26.8 6.8 246240 2 US-08-724-394A-22 Sequence 23, Appli 45 26.8 6.8 246240 2 US-08-724-394A-22 Sequence 23, Appli 28-26.8 6.8
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                          APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan TITLE OF INVENTION: Blackcurrant Promoters and Genes CORRESPONDENCE: 15
                                                                                                                                                                                                ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: NO. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/068,140A
; Sequence 9, Application US/09068140A; Patent No. 6281409
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C7/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1311 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribes nigrum
                                                                                                                                                                                                                                             CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 19406-0939
                                                        GENERAL INFORMATION:
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110 tcacagcaacaggcgcagggcctgcccacgccctttattttgcctgctacgaaagttaa 169
50 aggccctctggaggattataagaacggagggcctatggaggcccatgagggggctgaacg 109
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                                         3391 AAGCCCTTGGGTCGATACTGAAAGTTGAAGGTCCCGCCGGACTTTACCGTGGCATTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.1%; Score 32; DB 2; Length 1643; Best Local Similarity 49.4%; Pred. No. 0.29; Matches 83; Conservative 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN REGULATORY MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF-0356 US
                                                                                                                                                                                                                                                                                                               Sequence 68, Application US/08933750C Patent No. 5932442
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATY
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          September 23, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRAX: 415-845-4166
                                                                                                                                                                                                             3511 AGGAGACTTTTTCTCATG 3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                    170 aaaagacattgagtgatg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lal, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94304
                                                                                                                                                                                                                                                                                             US-08-933-750C-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CLONE: 72.
US-08-933-750C-68
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                                                                                                          50 aggccctctggaggattataagaacggagggcctatggaggcccatgagggggctgaacg 109
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                                                                                                                                                                                                               227 AAGCCCTTGGGTCGATACTGAAAGTTGAAGGTCCCGCCGGACTTTACCGTGGCATTGGTG 286
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                     Length 1311;
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                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                                                                                                                                             US-09-068-140A-14
Sequence 14, Application US/09068140A
Sequence 14, Application US/09068140A
GENERAL INFORMATION:
APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
APPLICANT: and Rex Michael Brennan
TITLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                     Score 32.4; DB 4;
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: SmithKline Beecham Corporation 709 Swedeland Road
                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70237
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFRAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                       8.2%;
                                                                                                                                                                                                                                                                            170 aaaagacattgagtgatg 187
                                                                                                                                                                                                                                                                                                        347 AGGACACTTTTCTCATG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 5150 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Ribes nigrum
                                      Best Local Similarity 52.2
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 709 Swedeland
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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Best Local S
                         Query Match
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86 ggaggcccatgagggggctgaacgtcacagcaacaggcgcagggcctgcccacgcccttt 145
                                    542 GGACCCICIGGAGCGGCCICCCCGCCACCTGGTGAIGACIGIGCCAGCIACCGCCAICI 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 ggaggcccatgagggggctgaacgtcacagcaacaggcgcagggcctgcccacgcccttt 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        503 GNAARGCNYTNAARGGNATGAAYATGAARGARATHAARGGNMGNACNGTNGCNGTNGAYT 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 attttgcctgctacgaaaagttaaaaaagacattgagtgatgtaatccaccctgggggca 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 GGGCNGTNGCNAARGAYAARTAYAARGAYACNCARWSNGTNWSNGCNATHGGNGARGARA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atagecatattgecaatggtgeggeegggtgtgtgtggeaacattaetteatgatgeageea 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             623 ARWSNCAYGARWSNAARCAYCARGARWSNGTNAARAARAARGGNMGNGARGARGARGAYA 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgaaccetgeggaaggtaatgatteeteaacetateaetetgtgggcagetgcacetgta 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                   146 attttgcctgctacgaaaagttaaaaaagacattgagtgatgtaatcc 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                   E: Science & Technology Law Group
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.6%; Score 30.2; 27.4%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                             Sequence 2, Application US/08676967
Patent No. 5747317
GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telome
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415)343.4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                     STREET: 268 Busn sur
CITY: San Francisco
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Best Local Similarity
Matches 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                  CA
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                                                                                                                                                                                                 US-08-676-967-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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482 CTACCCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAGGCACGAGGGCACCA 541
                                                              DB 3; Length 1643;
                                                                                                                                        146 attttgcctgctacgaaaagttaaaaaagacattgagtgatgtaatcc 193
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 3;
Pred. No. 0.29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0356 US
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APPLICATION NUMBER: US/08/933,7'
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   Sequence 68, Application US/09234613
Patent No. 6132973
                                                                                                                                                                                                                                                                                                            Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REG
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       Shah, Purvi
Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.1%;
Best Local Similarity 49.4%;
Matches 83; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
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STRANDEDNESS: singl
TOPOLOGY: linear
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LIBRARY: SYNOOAT01
CLONE: 724157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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US-09-234-613-68
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743 AYGAYGARGAYGARGARGARAAYATHGARWSNAARGTNACNAARCCNGT 794

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APPLICANT:
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; Pred. No. 1.5;
50; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,974
                                                                                                                                                                                                                                         ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                               APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                   Sequence 2, Application US/08676974
Patent No. 5770422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
ATTORNEY/ACENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 27.4%;
Matches 80; Conservative 5
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TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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US-08-676-974-2
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US-09-098-487-2
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GENERAL INFORMATION:

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APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 ggaggcccatgagggggtgaacgtcacagcaacaggcgcagggcctgcccacgcccttt 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2277;
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.6%; Score 30.2; DB 2; Best Local Similarity 27.4%; Pred. No. 1.5; Matches 80; Conservative 50; Mismatches 162;
                      TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UCB96-055
                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB9
TELECOMMUNICATION INFORMATION:
COLLINS, Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415)343.4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
FDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                              San Francisco
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                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                           94104
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,141
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APPLICATION NUMBER: US/08/202,389
FILING DATE: 28-FEB-1994
CLASSIFICATION: 435
                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: PERTYMAN, DAVIG G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEPAX: 404/688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08202389
Patent No. 5536636
    IBM PC compatible
                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 5532 base pairs TYPE: nucleic acid STRANDEDNESS: single
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                                                                                                    7 Jun 1995
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Best Local Similarity
                                                                                                        FILING DATE: 7
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION:
US-08-475-035-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              995 CGAGAACTGGAGCAGGCCATCCGGGGGCCGATGCCCAGGAGGACCTCAGGTGGTTCCGC 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 agaacggaggcctatggaggcccatgagggggctgaacgtcacagcaacaggggggg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 ctacagcctgacccagctgcccgctatcgcaatgtggtggaggccctctggaggattata 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KING, C. R.
APPLICANT: KING, C. R.
APPLICANT: KANG, WATTHIAS H.
APPLICANT: AARONSON, STUART A.
TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM
TITLE OF INVENTION: BGF RECEPTOR GENE
NUMBER OF SEQUENCES:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIF: 30303
ZIF: 30303
ZIF: 30303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 4091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Indels
                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-08/630,915A
FILING DATE: 03-08/630,915A
FILING DATE: 03-08/630,915A
ATOMNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET UNBER: 1101-174
TELEPHONE: (212) 790-9090
TELEFAX: (512) 869-8864/9741
TELES: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.5%; Score 29.6; Di
Best Local Similarity 51.5%; Pred. No. 3.2;
Matches 68; Conservative 0; Mismatches
                                                         12: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08475035 Patent No. 5985553
  USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                        Floppy disk
                                                                                               CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4091 bases
TYPE: nucleic acid
STRANDEDNESS: single
                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1115 CTCCCGCACACC 1126
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TITLE OF INVENTION:
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MOLECULE TYPE: DNA
                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-630-915A-33
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                                                                              STREET:
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258 tgcagccatgaaccctgcggaaggtaatgattcctcaacctatcactctgtgggcagctg 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4665 ACATTGGATTCATCAGCATTTGGACCAATAGCCCACAGCTGAGAATGTGGAATA 4718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Freeman Jr., Robert M.
APPLICANT: Plutzky, Jorge
APPLICANT: Neel, Benjamin G.
APPLICANT: Rosenberg, Robert D.
TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Pred. No. 5.2;
0; Mismatches
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100 gggctgaacgtcacagcaacaggcgcagggcctgcccacgccctttattttgcctgctac 159
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                                                                                                                                                                                                                                                               Score 29; DB 4; Length 8600;
Pred. No. 7.7;
0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMBUTER: TBM COMPAGE.
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OFFICE FASTSEO for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Angelika
TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7690 CTACAGACAAAGCTTAATCAAGTG 7666
                                                                                                                                                                                                                                                                                                                                                                                                                                            160 gaaaagttaaaaaagacattgagtg 184
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09073569
Patent No. 6084088
                                                                                                                                                                                                                                                                   7.3%;
58.8%;
             INFORMATION FOR SEQ ID NO: 1:
                               SEQUENCE CHARACTERISTICS:
LENGTH: 8600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                   Query Match 7.3
Best Local Similarity 58.8
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity
Matches 42; Conserva
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US-09-073-569-4
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CLASSIFICATION:
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US-09-457-708-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Swiatkowski, David J.
APPLICANT: Swiatkowski, David J.
APPLICANT: Sampson, Julian R.
APPLICANT: Povey, Sue
APPLICANT: Povey, Sue
APPLICANT: Halley, Dicky
TITLE OF INVENTION: Compositions and Methods Based U
TITLE OF INVENTION: Sclerosis-1 (TSC-1) Gene and Gene Product
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Indels
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ZIP: 20004-1008

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29; DB 1
Pred. No. 3.3;
0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI331/42002
TELECOMMUNCATION INFORMATION:
TELECOMMUNCATION 1000RAMATION:
TELEFHONE: (202) 639-6585
TELEFAX: (202) 639-6604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 ctacgaaaagttaaaaaagacattgagtgatgt 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 AGAGTCTCAGCCAACCTGGTGTTTTGTGTCTT 197
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
PELLING DATE: 26-UN-1991
FILING DATE: 26-UN-1991
ATTORNEY AGENT INFORMATION:
NAME: Grandhan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: B1H92-05MA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09457708
Patent No. 6326483
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.3%;
Best Local Similarity 57.0%;
Matches 53; Conservative
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2..1540
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                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY;
; LOCATION:
US-08-202-389-1
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64 attataagaacggagggcctatggaggcccatgagggggctgaacgtcacagca 117
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Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: Masayoshi MISHINA
TITLE OF INVENTION:
NUMBER OF SEQUENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%; Score 28.4; DB 1; Length 4446; 70.4%; Pred. No. 8.8; tive 0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MS-DOS V.5

OFFRATING SYSTEM: MS-DOS V.5

SOFTWARE: WORD Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/026,138E

FILING DATE: 26-FEB-1993

PROOF APPLICATION NUMBER: JP 19353/1992

FILING DATE: 26-FEB-1992

APPLICATION NUMBER: JP 173155/1992

FILING DATE: 36-JUN-1992

APPLICATION NUMBER: JP 215017/1992

FILING DATE: 12-AG-11992

APPLICATION NUMBER: JP 215017/1992

FILING DATE: 13-NOV-1992

APPLICATION NUMBER: JP 20-JUN-1992

APPLICATION NUMBER: JP 20-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE: Drain
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 to 444
US-08-026-138E-6
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Nishiohata Residence 1-107
STREET: 5214, Nishiohata-machi
CITY: Niigata-shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 96-2340
TELEFAX: (212) 953-7733
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: 22,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4446 nucleic acids
TYPE: nucleic acid
STRANDEDNESS: double strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 70.4 nes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Nijgata-ken
COUNTRY: JAPAN
ZIP: 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA
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ORIGINAL SOURCE:
                                                                                                                                       RESULT 14
US-08-026-138E-6/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-268-163-9/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                     170 aaaagacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggtgcgg 229
                            626 ARRAARTCYTINCKRTIRCARTIYICNGTCAINCCNACNGGNCCDAIYICYTGNGINCCR 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08026138E
Sequence 17, Application US/08026138E
Sequence 17, Application US/08026138E
Sequence 17, Application US/08026138E
SEQUENCE MASSAGE
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Nishlohata Residence 1-107
STREET: 5214, Nishlohata-machi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.2%; Score 28.4; DB 1; Length 4368; 70.4%; Pred. No. 8.7; tive 0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 951
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17: FROM 1 to 4368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB-1993
APPLICATION NUMBER: JP 39563/1992
FILING DATE: 26-FEB-1992
APPLICATION NUMBER: JP 173155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: 23,389
REFERENCE/DOCKET NUMBER: F-4551
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4368 nucleic acids
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Nishiohata Residence 1-107
STREET: 5214, Nishiohata-machi
CITY: Nilgata-shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS-DOS V.5
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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TISSUE TYPE: brain
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
                                                                                                                                                                                                                290 cctcaacctatcactct 306
                                                                                                                                                                                                                                                              506 CCNCCNCCNARNCK 490
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Best Local Similarity 70.4
Matches 38; Conservative
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COUNTRY: JAPAN
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Gaps

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Sequence 9, Application US/09268163B
Patent No. 6353091
GENERAL INFORMATION:
APPLICANT: Lipscombe, Diane
APPLICANT: Lipscombe, Diane
APPLICANT: Lipscombe, Diane
APPLICANT: Lipscombe, Diane
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
FILE REPERENCE: B1055/7000
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US/09/268,163B
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 7011
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: 1.7008
US-09-268-163-9
US-09-268-163-9

QUERY MATCh
MATCHES 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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167 taaaaaagacattgagtgatgtaatccacctgggggcaatagccatattgccaatggtg 226 i il ilii i i i ii i i i i i i i i i 6 6357 TGAAGAAGAGGAGGAGGCTCCCTGGGGACCGGCCTCGTTACGTTACGCTC 6298

da ya

Search completed: September 28, 2002, 07:56:08 Job time: 11253 sec

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AK015770 Mus muscu
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BG895490 358967 MA
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AZ693917 AST-2HLB2
                                                                                                                                                                                                                                                                                                                                                              603077989F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5169694 5', mRNA sequence.
                                        AV704087 AV704087
B148355 dac73b07.
AL654963 AL654963
AA104365 mp01g06.r
BE014800 126651 MA
A1942584 fc73c03.y
BB654057 BB654057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 747)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: capDS-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can if Clone distribution. MGC clone distribution information can http://image.llnl.gov
Plate: LLAMI1422 row: a column: 23
High quality sequence stop: 743.
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/clone_lib="NIH_MGC_119"
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/lab_host="DH108"
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BJ035232
BJ012200
AW210205
AI33696
AI33696
AI310713
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BG777404
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AA061624
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BJ039504
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BI448355
AL654963
AA104365
BE014800
AI942584
BB654057
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BI827322.1 GI:15938872
 Homo sapiens
                       human.
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129.6
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
SOURCE
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 ; Search time 4881.77 Seconds (without alignments) 1094.848 Million cell updates/sec
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B1045863 WR3 FN020
B1541703 455541 MA
BE913718 601669072
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BH81943 603076873
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BF916224 CM2-UT011
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BI739710 603361983
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                                                                                                                                      1 atgcagagtctacagcctga......ttaccttgttttaccactag 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                       13736207 seqs, 6748477542 residues
                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                       September 28, 2002, 06:22:49
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Maximum Match 100%
Listing first 45 summaries
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B1541703
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BG964218
BG295496
B1794616
B1794616
B1185580
AW211366
B1831943
                                                   OM nucleic - nucleic search, using sw model
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BM488747
BF916224
BI412175
BI739710
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Gapop 10.0 , Gapext 1.0
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396
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2577.6
265.8
265.8
246.4
246.4
2246.4
2244.8
224.4
222.3
42.5
223.4
195.4
195.4
195.4
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Minimum DB Maximum DB

Database

Sequence:

Run on:

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Result

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Homo saplens
                                                           Similarity
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                                            Query Match
Best Local Simi
Matches 278;
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AUTHORS
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COMMENT
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BI045863
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               888 bp mRNA linear EST 13-FEB-2001 ALS30804 LTI_NFL001_NBC4 Homo sapiens cDNA clone CSODD008YH17 5 ALS30804
0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NHWC Library." I others
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1. (bases 1 to 888)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                             1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg
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BP 191 91006 EVRY cedex - France
Email: segrefégenoscope cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                   ö
                                                                                                                    Length 747;
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="neuroblastoma cells"
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0
                                                                                                                    core 280; DB 10;
Pred. No. 6.2e-78;
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100.0%; Pred. No. 6.2
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                                                                                                                                     Best Local Similarity 100.
Matches 280; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 480)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-FN0209-
3000li-004-hi0&ta3=2001-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 480.
Location/Qualifiers
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MRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                  417 ATGCAGAGTCTACAGCCTGACCCAGCTGCCGCTATCGCAATGTGTTGGAGGCCCTCTGG 476
                                                                                                                                                                                                                                                                                                    ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
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                                                                                                    atgcagagtctacagcctgacccagctgccogctatcgcaatgtgttggaggccctctgg
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI045863 480 bp mRNA linear MR3-FN0209-300101-004-h10 FN0209 Homo sapiens CDNA,
     Length
                                                 Indels
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Pred. No. 3.8e-77;
1; Mismatches 1;
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/db_xref="taxon:9606"
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70.1%;
ilarity 99.3%;
Conservative
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/clone_lib="MARC 1BOV"
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Matches 265; Conservative
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BE913718
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                   Length 480;
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                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 ggcaacattacttcatgatgcagccatgaacctgcggaag 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 GGCACCATTACTTCATGATGCAGCCATGAACCCTGCGGAAG 354
                                                                                                                               DB 10;
                                                                                                                               Score 265.8; DB 10;
Pred. No. 1.8e-73;
0; Mismatches 2;
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/db_xref="taxon:9913"
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Location/Qualifiers
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Best Local Similarity 98.9%;
Matches 278; Conservative
                                                                126 c
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National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov, Ph.D.

Email: cgapbs-remail cilbert Smith, Ph.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Prayed by: The I.N.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.N.A.G.E. Consortium/LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 598)
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
/inche="vector: pCMV sported tissue from lymph node, ovary, fat, hypothamus, and pituitary."
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/db_xref="taxon:10090"
/clone="IMAGE:3969256"
/clone=lib="NCI_CGAP_MamI"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                Score 256; DB 10;
Pred. No. 2.4e-70;
0; Mismatches 15;
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Plate: LLAM9146 row: 0 column: 17
High quality sequence stop: 593.
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94.6%;
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62.2%; Score 246.4; DB 10; Length 1131;
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                                                               Similarity
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                                                 Query Match
Best Local Simi
Matches 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-framiliningov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium/LLNL at:
thus distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
thtp://image.lln.gov
Plate: LLAMIO98 row: p column: 24
High quality sequence start: 2
High quality sequence stop: 632.
Location/Qualifiers

ree
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/clone_lib="NCI_CGAP_CO24"
/lab_host="DHIOB (TI_phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 645)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Primer: Oligo dT
              Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 175\ c 172\ g 110\ t
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0
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Site_2: NotI; Cloned unidirectionally.
                                                                                                                    DB 10;
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92.5%; Pred. No. 2.8e-67;
ive 0; Mismatches 21
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/strain="FVB/N"
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                                                                                                                                                       Matches 259; Conservative
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BG964218
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AUTHORS
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
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/tissue_type="retina"
/lab_host="PuHl0B (phage-resistant)"
/lab_host="PuHl0B (phage-resistant)"
/lab_host="PuHl0B (phage-resistant)"
/note="Organ: eye: Vector: pCMV-SPORT6; Site_1: Not1:
Site_2: Sall; Cloned unidirectionally; oligo-dr primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602392826F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4504638 5' mRNA sequence.
BG295496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incytte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                       61 aggattataagaacggaggcctatggaggcccatgaggggctgaacgtcacagcaaca 120
                                                                                                                                                                                                                                                                                                                                    ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
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645;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Score 246.4; DB 1 Pred. No. 2.9e-67;
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Plate: LLAM10377 row: c column: 07
High quality sequence stop: 753.
Location/Qualifiers
                                                   0; Mismatches
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/db_xref="taxon:10090"
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/clone_lib="NIH_MGC_94"
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62.2%;
ilarity 92.5%;
Conservative
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GI:14659989
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Best Local Similarity 92.1%;
Matches 258; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dasss 1 to 560)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Schmitt, A., Theising, B., Ritter, E., Martin, J., Blistain, A., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Williams, T., Endokson, Y. and Bowers, T., Stagareishvili, R., Williams, T., Endokson, Y. and Bowers, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 430.
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adult, mixed"
                                                                                                                     440
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N1-MMS1"
                                                                                                                                                                                                                                                           Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                          .1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgtggaggccctctgg
                  Indels
                                                                                                                                                                                                                                                                                                                                                 241 gcaacattacttcatgatgcagccatgaacctgcggaag 280
 Pred. No. 3.5e-67
                  0; Mismatches
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
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BI794616
BI794616.1 GI:15822341
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Other_ESTs: ic92e02.x1
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92.58;
                  Conservative
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/note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I; Five libraries representing EIO:5/12.5 pancreatic bud, EI6.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts: The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Scares 1956 Genome Research 6:791-806; O.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
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Sus.
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1 (bases 1 to 574)
Caetano,A.R., Johnson,R.K. and Pomp,D.
Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles
Unpublished (2001)
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UNL-P-FN-cy-f-02-0-UNL.sl UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-cy-f-02-0-UNL 3', mRNA sequence.
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Pred. No. 8.8e-67;
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Department of Animal Science
University of Nebraska, Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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Conservative
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                                                                                                              /clone_lib="UNL-r ...
/dev_stage="ADULT"
/lab_host="Deta" Thing Table Technologies)" with a modified
/hote="Vector: pT/T3D-Pac (Pharmacia) with a modified
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_l: ECO RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and ther
nucleotides present between the Not I site and ther
-linc-dT track. The library was constructed as described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NALILIDO SOL DE MRNA LINEAR EST 03-DEC-1999 UO80b07.yl NCI_CGAP_Mam3 Mus musculus CDNA clone IMAGE:2648821 5/ similar to WP:W02B12.9 CE03769 MITOCHONDRIAL RNA SPLICING MSR4 LIKE PROTIEIN ;, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 501)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                /strain="University of Nebraska, Lincoln Swine Selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtg 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 ANAACATTACTTCATGATGCAGCCATGAATCCAGCAGAAG 413
                                                                                                   /clone="UNL-P-FN-cy-f-02-0-UNL"
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 244.6; DB Pred. No. 1e-66; 0; Mismatches
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                                    scrofa"
                                                                                   /db_xref="taxon:9823"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    TAG_SEQ=None found"
171 c 165 g
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                                  /ordanism="Sus
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Stle_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 23, 37-43 (1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 701)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Mam3"
/tissue_Ypp="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 234; DB 9;
Pred. No. 2.3e-63;
0; Mismatches 20;
                                                                                                                                                                                                                                                                             1. :501
/organism="Mus musculus"
/strain="129 - C57/B6 - Fv
/db_xref="taxon:10090"
/clone="IMAGE:2648821"
                                                                                                                                                                                             Seq primer: -40RP from Gibco
High quality sequence stop: 427
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Mus musculus
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                                                                                                                                                                                                                                                                                                /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA Source normal medulla from annonymous male age 27. Library is oligo-dT prinned and directionally cloned (EcoRV site is destroyed upon colning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NILMGC Library."
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., 'Chitko-McKown, C.G.,
Feetea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.a column: 20
High quality sequence start: 29
High quality sequence stop: 699.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 701;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             אפסבעה 336 bp mRNA linear 19106 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW326482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:5168539"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH108"
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggattataagaacggaggcctatggaggcccatgagggggctgaacgtcacagcaaca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 AGGATTATAAGAACGGAGGGCCTGTGGAGGCCCATGCGAGGCCTGAACGTCACAGCAACA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgttggaggccctctgg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 223.4; DB 9; Length 336;
Pred. No. 4.7e-60;
0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
                     at Animal Research Center
Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 8 row: F column: 16
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                 1. .336
/organism="Bos taurus'
                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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PCR PRimers
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                USDA, ARS, US Meat A
PO Box 166, Clay Cen
Tel: 402 762 4366
Fax: 402 762 4390
Contact: Smith TPL
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BI103329
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                                                                                                                                                                                                     /clone="IMAGE:5043992"
/clone_lib="NOT_CGAP_Kid14"
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/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pgm2n.pk008.12 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk008.12 5' similar to ref[XP_050766.1 (XM_050766) putative mitochondrial solute carrier [Homo sapiens] gplAAK49519.1|AF327402.1 (AF327402) putative mitochondrial solute carrier Elmo sapiens] gplAAK49519.1|AF327402.1 (AF327402) putative mitochondrial solute Garrier splice variant [Homo sapiens], mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus
Kubaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 546)
Cogburni.A. and Monsonego-Ornan,E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
row: 1 column: 09
High quality sequence stop: 777.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                             Length 817;
                                                                                                                                                                                                                                                                                                                                                                                          56.3%; Score 222.8; DB 10; Length ilarity 91.5%; Pred. No. 9.9e-60; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
                                                                                                                                                                      /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM488747.1 GI:18609678
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                                                                                                                                                                                                                                                                                                                                                                                                                           258;
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                             BASE COUNT
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TITLE
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fissue type="Breast muscle, leg muscle and epiphyseal growth plate"

/dev_stage="Breast.leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coll EMDH10B"
/note="Vector: pcMvSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 agtgatgtaatccaccctgggggcaatagccatattgccaatggtgcggccgggtgtgtg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 aggattataagaacggaggcctatggaggcccatgaggggggctgaacgtcacagcaaca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 AGCGACGTCATCCACGCGGGGGCAATAGCCATGTGGCNNNCGGTGCAGCCGGGTGTGTA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                               Ottawa Res. Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 ATGCAGAGCCTGCGGCCCGAGCCCGCCGCCGCTACCGCAACGTGCTGGAGGCCCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="pgm2n.pk008.12"
/clone_lib="Normalized Chicken Breast Muscle, Leand Epiphyseal Growth Plate cDNA library (pgm2n)
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.3%; Score 195.4; DB 10; Length 546; 80.7%; Pred. No. 4.5e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                       www.chickest.udel.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                               and
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0; Mismatches 54
                                                                                                                                                                             /strain="Commercial broiler
Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 t
                                                                                                                                                     /organism="Gallus gallus"
                                                                                                                                                                                                                               /db_xref="taxon:9031"
                                                                       gburn@udel.edu, www
Location/Qualifiers
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                                                                       Email: cogburn@udel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 80.7 Matches 226; Conservative
                  Tel: 302-831-1335
Fax: 302-831-2822
Townsend Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence tags
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone_lib="UT0112"
/dclone_lib="UT0112"
/doc="Organ: uterus_tumor; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
Site_1: SmaI; A mini-library was made by cloning products
Site_2: Lidwig Institute for Cancer Research)
profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-270701
Fa
                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 gaacggagggcctatggaggcccatgagggggctgaacgtcacagcaacagggcgcgggc 130
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     Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Best Local Similarity 97.6%; Pred. No. 6.8e-50;
Matches 205; Conservative 0; Mismatches 4
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125 c 126 g 90 t
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